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RESULT 2
ID O42324 PRELIMINARY; PRT; 383 AA.
AC O42324;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MU-OPIOID RECEPTOR.
OS CATOSTOMUS COMMERSONI (WHITE SUCKER).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; COBITOIDEA;
OC CATOSTOMIDAE; CATOSTOMUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA DARLISON M.G., HARVEY R.J., GRETEN F.R., KREIENKAMP H.J., ZWIERS H.,
RA STEHMER T., LEDERIS K., RICHTER D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; Y10904; E1169530;
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm1.1;
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 383 AA; 43232 MW; 00BDBCBD CRC32;

Query Match 65.5%; Score 1461; DB 13; Length 383;
Best Local Similarity 65.1%; Pred. No. 1.22e-212; Indels 6; Gaps 4;
Matches 183; Conservative 50; Mismatches 42;

Db 85 YTKMTATNIYIFNLADALATSTLPQSVNYLMGWPQGVCKIVMSIDYNNFTSI 144
QY 1 YTKMTATNIYIFNLADALATSTLPQSVNYLMGWPQGVCKIVMSIDYNNFTSI 60
Db 145 FTLTMSVDRIYAVCHPVKALDFTPLKAKIINICWLLSSVGSIAVLGGTKVRE 204
QY 61 FTLTMSVDRIYAVCHPVKALDFTPLKAKIINICWLLSSVGSIAVLGGTKVRE 118
Db 205 PLOVSNFDCITLFPHPPW-YNETLKICVFTLAIMPVLIITVCYGLMILRLKSVMLSG 263
QY 119 -VDV-IECCLOFPDDYSWDLFMKICVFIFAFVPLIIIVCYTLMILRLKSVMLSG 175
Db 264 SREKDNRLRRITRMVIVVAVFICWTPHIFVTKALVTPNSLFTQVWHFCAIGYT 323
QY 175 SREKDNRLRRITRMVIVVAVFICWTPHIFVTKALVTPNSLFTQVWHFCAIGYT 235
Db 324 NSCLAPVYAFDENFKRCFREFCVPSVYLDLQNSTNSN 364
QY 236 NSCLAPVYAFDENFKRCFREFCVPSVYLDLQNSTNSN 276

RESULT 3
ID O60733 PRELIMINARY; PRT; 117 AA.
AC O60733;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OPIOID RECEPTOR, KAPPA 1 (KAPPA OPIOID RECEPTOR) (FRAGMENT).
GN OPRK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC GRANDY D.K.;
RA SUBMITTED (NOV-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; U16998; G595937;
DR MGD; MGI:97439; OPRK1.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm1.1;
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT NON_TER 1
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FT NON_TER 117
SQ SEQUENCE 117 AA; 13070 MW; FCCF68E1 CRC32;

Query Match 38.4%; Score 856; DB 11; Length 117;
Best Local Similarity 96.6%; Pred. No. 5.58e-113; Indels 0; Gaps 0;
Matches 113; Conservative 3; Mismatches 1;

Db 1 YTKMTATNIYIFNLADALATSTLPQSVNYLMGWPQGVCKIVMSIDYNNFTSI 60
QY 1 YTKMTATNIYIFNLADALATSTLPQSVNYLMGWPQGVCKIVMSIDYNNFTSI 60
Db 61 FTLTMSVDRIYAVCHPVKALDFTPLKAKIINICWLLSSVGSIAVLGGTKVRE 117
QY 61 FTLTMSVDRIYAVCHPVKALDFTPLKAKIINICWLLSSVGSIAVLGGTKVRE 117

RESULT 4
ID Q64206 PRELIMINARY; PRT; 119 AA.
AC Q64206;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA OPIOID RECEPTOR/DOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 96211968.
RA ROY S., SEDAI M., RAMAKRISHNAN S., BARKE R.A., LOH H.H.;
RT "Differential effects of opioids on the proliferation of a macrophage
cell line, Mac 1.2F5."
RL CELL. IMMUNOL. 169:271-277 (1996).
DR EMBL; S81965; E257299;
DR PFAM; PF00001; 7tm1.1;
FT NON_TER 1
SQ SEQUENCE 119 AA; 13380 MW; DFC85C30 CRC32;

Query Match 28.8%; Score 643; DB 11; Length 119;
Best Local Similarity 66.9%; Pred. No. 1.23e-78;
Matches 81; Conservative 18; Mismatches 19; Indels 3; Gaps 3;

Db 1 IFTLTMSVDRIYAVCHPVKALDFTPLKAKIINICWLLSSVGSIAVLGGTKVRE 60
QY 60 IFTLTMSVDRIYAVCHPVKALDFTPLKAKIINICWLLSSVGSIAVLGGTKVRE 119
Db 61 -LV-CMLQFPSPW-WDITVKICVLFPAFVVPILIIITVCYGLMILRLKSVMLSGSREK 117
QY 120 DVEICLOFPDDYSWDLFMKICVFIFAFVPLIIIVCYTLMILRLKSVMLSGSREK 179
Db 118 D 118
QY 180 D 180

RESULT 5
ID O76873 PRELIMINARY; PRT; 263 AA.
AC O76873;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE EG-121E7.2 PROTEIN.
GN EG-121E7.2.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RA MURPHY L., HARRIS D., BARRELL B.;
RT "Sequencing the distal X chromosome of Drosophila melanogaster."
RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
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OC CATARRHINT; HOMINIDAE; HOMO.

CATARRHINI; HOMINIDAE; HOMO.

C CATARRHINI; HOMINIDAE; HOMO.

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RN      SEQUENCE FROM N.A.
RA      ZHANG L., CARROTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RL      H.O.D.D.;
RL      AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR      EMBL; AF011536; G2305190; -.
DR      EMBL; AF011516; G2305150; -.
DR      EMBL; AF011534; G2305186; -.
DR      PFAM; PF00001; 7tmL3; 1.
FT      NON_TER 352
SQ      SEQUENCE 352 AA; 40552 MW; BIECA8D9 CRC32;

Query Match      20.7%; Score 461; DB 4; Length 352;
Best Local Similarity 28.2%; Pred. No. 5.78e-50;
Matches 74; Conservative 84; Mismatches 88; Indels 16; Gaps 14;

Db 60 RLKMTDIYLLNLAISDFLLTVTF-WAHYAAQWDFGNMQLGLFYIGFFSGIFF 118
QY 3 KMKIATNIYIFNLADALVTTMPFQSTVYIMNSWPFQGLVCKIVISIDYNNFTSIPT 62

Db 119 IILLIDRLVAVHAEKAKRTVTGVTSVITVWVAVFASLPGIIFTSQ-KEGLHYT 177
QY 63 IYMSVDRIAVCHPKALDERTPLKAKIINICIWLLSSVSGISAIVLGTKVREDVDVI 122

Db 178 -CSSHPYSQYQWKNFOTLKIIVLGLVPLLVVICYS-GIL-KT--LLR-CRN-EKK 229
QY 123 ECOLQPPDDYSWDLFNKICVFIFAVIPVLIIVCYTLMILRLKXVRLLSGSRKDXN 182

Db 230 RHRAVELIETIMVYELFWAPNIVLLNLTQEFPGNCCSSNRDLQAMQVETLGMTH 289
QY 183 LRIRLVLVVAVFVVCWTPHI--FIL-V-EAL-G-STSHSAALS-SYFICIALGYIN 236

Db 290 CCINPIIYAFVGEKFNLYLVF 311
QY 237 SSINPIIYAFLDENFKRCFRDF 258

RESULT 15
ID O60755 PRELIMINARY; PRT; 368 AA.
AC O60755;
DT 01-AUG-1998 (TREMELREL. 07, CREATED)
DT 01-AUG-1998 (TREMELREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
DE GALANIN 2 RECEPTOR HOMOLOG.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-UTERUS;
RA BENNETT M.M., LESCOE M.K., GALLIPOLI P.2., RAMASHADRAN T.V.;
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98389766.
RA SMITH K.E., WALKER M.W., ARTYMSHYN R., BARD J., BORONSKY B.,
RA TAMM J.A., YAO W.-J., VAYSSE P.J.-J., BRANCHEK T.A., GERALD C.,
RA JONES K.A.;
RT "cloned human and rat galanin GALT3 receptors. Pharmacology and
RT activation of g-protein inwardly rectifying k+ channels.";
RL J. BIOL. CHEM. 273:23321-23326(1998).
DR EMBL; AF067733; G3176927; -.
DR EMBL; AF073795; G3608410; -.
SQ SEQUENCE 368 AA; 39573 MW; 2DF74618 CRC32;

Query Match      20.7%; Score 461; DB 4; Length 368;
Best Local Similarity 31.0%; Pred. No. 5.78e-50;
Matches 88; Conservative 76; Mismatches 106; Indels 14; Gaps 10;

Db 55 STTDLFILNVLADICFLCCVPGQATVITLDAWLFGLVCKAVHLLIYLYTWASSFTLA 114
QY 6 TAINIYIFNLADALVTTMPFQSTVYIMNSWPFQGLVCKIVISIDYNNFTSIPT 64

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Db 115 AVSDRYIAVHPLRSALRTEFENARAAYGL-VWLLAALFSAPILSYIGT-VR--YGALE 170
QY 65 MMSVDRYIAVCHPKALDERTPLKAKI-INICIWLLSSVSGISAIVLGTKVREDVDVIE 123

Db 171 LCVPAWEDA-RRAL--DVATFAGYLLPVAVVSLAYGTLRFLNAAVGPAGAAAAEARR 227
QY 124 CCLOFPDDYSWDLFNKICVFIFAVIPVLIIVCY--TLMILRLKXVRLLSGSR-KD 180

Db 228 RATGRAGRAMLAVALYALCWGPHALILCTWYGRFAFSPATYACRLASHCHLAYANSCIN 287
QY 181 XNLRIRITRLVAVVAVFVVCWTPHIHIFILVEALGSTSHSTAALSSSYFICIALGYINSSLN 240

Db 288 PLVYALASRHFRAFRFLWPCGRRRRHRARLRVRFPASSGPP 331
QY 241 PILYAFLDENFKRCFRDF--CFPLKMMXKSTSRVRNIVQDPA 282

Search completed: Thu Feb 17 11:17:01 2000
Job time : 25 secs.

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GenCore version 4.5
 Copyright (c) 1993 - 1998 CompuGen Ltd.
 OM nucleic - nucleic search, using sw model
 Run On: February 17, 2000, 09:39:05 ; Search time 66.73 seconds
 (without alignments)
 5286.540 Million cell updates/sec

Title: US-08-455-683-1
 Perfect score: 1410
 Sequence: 1 GCGCAGCTTGTGATGCCAA.....AACCCAGATTACAACTGCAG 1410

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36.*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1410	100.0	1410	1	Q75926 Mouse kappa opioid
2	1408	99.9	1408	1	V49254 Mouse kappa opiate
3	125	8.9	2481	1	Q86725 Mammalian kappa op
4	77	5.5	1275	1	T32601 Human kappa opioid
5	32	2.3	1000	1	T95931 Human kappa opioid
6	32	2.3	1142	1	T12550 Human kappa opioid
7	32	2.3	1143	1	T90998 Human kappa opioid
8	32	2.3	1284	1	T90999 Human kappa opioid
9	31	2.2	2447	1	C56702 Human kappa opioid
10	29	2.1	822	1	Q92156 Partial sequence o
11	25	1.8	1330	1	Q75928 Brain somatostatin
12	25	1.8	1567	1	Q89233 Mouse opioid recep
13	25	1.8	2600	1	Q90096 Rat opioid recepto
14	25	1.8	2706	1	Q92972 Mouse kappa-3 opio
15	25	1.8	1452	1	T89585 Rat opiorph recept
16	25	1.8	1452	1	T90381 Rat orphanin FQ re
17	25	1.8	1452	1	T89585 Rat methadone-spec
18	23	1.6	1821	1	V56017 Sequence of murine
19	23	1.6	2216	1	Q66556 Murine delta opioi
20	23	1.6	2272	1	Q75927 Mouse delta opioi
21	23	1.6	2218	1	V49253 Mouse delta opiate
22	20	1.4	2070	1	Q79199 Rat mu-subtype opi
23	20	1.4	1618	1	Q89222 Rat mu opioid rece
24	20	1.4	1618	1	Q89223 Transcription regu
25	20	1.4	1610	1	Q89226 Human mu opioid re
26	20	1.4	2160	1	Q93102 Human mu opiate re
27	20	1.4	36	1	T12551 Human kappa opioi
28	20	1.4	39	1	T12554 Human kappa opioi
29	20	1.4	2162	1	V61985 Human mu-opioid re
30	20	1.4	2162	1	V61984 Human mu-opioid re
31	20	1.4	2162	1	V61986 Human mu-opioid re
32	20	1.4	2162	1	V61987 Human mu-opioid re
33	20	1.4	2162	1	V61988 Human mu-opioid re
34	20	1.4	2162	1	V61989 Human mu-opioid re
35	20	1.4	2162	1	V61990 Human mu-opioid re
36	20	1.4	2162	1	V61991 Human mu-opioid re
37	20	1.4	2162	1	V61992 Human mu-opioid re
38	20	1.4	2162	1	V61993 Human mu-opioid re
39	20	1.4	2162	1	V61994 Human mu-opioid re

40	20	1.4	2162	1	V61995 Human mu-opioid re
41	18	1.3	829	1	Q56703 Partial sequence o
42	18	1.3	403	1	X39521 Human secreted pro
43	17	1.2	7960	1	N90568 Ovine Y-chromosom
44	17	1.2	11715	1	N81564 Genomic sequence e
45	17	1.2	11724	1	N70102 Complete genomic s

ALIGNMENTS

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RESULT 1
Q75926
ID Q75926 standard; DNA; 1410 BP.
AC Q75926;
DT 17-AUG-1995 (first entry)
DE Mouse kappa opioid receptor MORK1 cDNA.
KW Mouse; Kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 186..1328
FT tag= a
FT product= mouse kappa opioid receptor
W09428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100594.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03..
DR P-PSDB; R67669.
DR Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 10; Page 207-211; 300pp; English.
CC MORK1. The gene was isolated from the novel mouse kappa opioid receptor gene
CC fragment (amplified from the cDNA library with primers 075929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SSTR) receptor
CC kappa opioid receptor clone, lambda msl-1. The 1.2 kb PstI fragment from the mouse
CC promoter-based expression vector pCMV-8b. The resultant construct
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete.
CC truncated or chimaeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

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Query Match 100.0%; Score 1410; DB 1; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCAGCTTGTGATGCCAAACAGGAGAGCTTCTTCCAGTCTTGAAGGCAAAATTGA 60
Db 1 GCGCAGCTTGTGATGCCAAACAGGAGAGCTTCTTCCAGTCTTGAAGGCAAAATTGA 60
QY 61 GCATCAGGACGTGGACCCATCAGGCTGAACAGCTACTCAGGATCTAAAGTGTGACTT 120
Db 61 GCATCAGGACGTGGACCCATCAGGCTGAACAGCTACTCAGGATCTAAAGTGTGACTT 120
QY 121 GGAAAGCTGACGGTGTGACTTGGGAGGAGGAGGTGCCAATCAGGATCTGGAGTGCAGGCG 180
Db 121 GGAAAGCTGACGGTGTGACTTGGGAGGAGGAGGTGCCAATCAGGATCTGGAGTGCAGGCG 180

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QY 243 GCTTGGCTTCICCCCAACAGCAGCTCTTGGTTCCCAACTGGGCGAGATCCGACAGTAAT 302
Db 241 GCTTGGCTTCCTCCCAACAGCAGCTCTTGGTTCCCAACTGGGCGAGATCCGACAGTAAT 300
QY 303 GGCAGTGTGGGCTCAGAGATCAGAGCTCAGAGCTGGAGTCCGCGACATCTCCCGGCAATCCCT 362
Db 301 GGCAGTGTGGGCTCAGAGATCAGAGCTCAGAGCTGGAGTCCGCGACATCTCCCGGCAATCCCT 360
QY 363 GTTATCATCACCGCTGTCTACTCTCTGTGTATTTGTGGGGCTTAGTGGGCAATTCCTG 422
Db 361 GTTATCATCAOCCGTGTCTACTCTCTGTGTATTTGTGGGGCTTAGTGGGCAATTCCTG 420
QY 423 GTATGTTTGTCAATCCGATACAGAGATGAGACCGCAACCAACATCATACATATTT 482
Db 421 GTCAATGTTTGTCAATCCGATACAGAGATGAGACCGCAACCAACATCATACATATTT 480
QY 483 AACTGGCTTTGGCAGATGCTTTTGTGTACTACCACTATGCGCTTTCAGAGCTGTCTAC 542
Db 481 AACTGGCTTTGGCAGATGCTTTTGTGTACTACCACTATGCGCTTTCAGAGCTGTCTAC 540
QY 543 TTGATGAATCTTGGCCCTTTGGAGATGTCTATGCAAGATGTCAATTCATTGACTAC 602
Db 541 TTGATGAATCTTGGCCCTTTGGAGATGTCTATGCAAGATGTCAATTCATTGACTAC 600
QY 603 TACAACATGTTTACCAGCATATTCACCTTGACCATGATGATGTGGACCGCTACATGCT 662
Db 601 TACAACATGTTTACCAGCATATTCACCTTGACCATGATGATGTGGACCGCTACATGCT 660
QY 663 GTGTGCCACCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAAGATCATCAAC 722
Db 661 GTGTGCCACCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAAGATCATCAAC 720
QY 723 ATCTGATTTGGCTCTCGCATCATCTGTTGGTATATACAGCATAGTCCTTTGGAGCAC 782
Db 721 ATCTGATTTGGCTCTCGCATCATCTGTTGGTATATACAGCATAGTCCTTTGGAGCAC 780
QY 783 AAAGTCAGGAAGATGTGGATGTCATTAAGATCTCTCTGCTTTGCTTTGATGATGAATAT 842
Db 781 AAAGTCAGGAAGATGTGGATGTCATTAAGATCTCTCTGCTTTGCTTTGATGATGAATAT 840
QY 843 TCCTGTGGGATCTCTTCAATGAGATCTGTGCTTCTGCTTTGCTTTGATGATGAATAT 902
Db 841 TCCTGTGGGATCTCTTCAATGAGATCTGTGCTTCTGCTTTGCTTTGATGATGAATAT 900
QY 903 CTCATCATCTGCTCTACACCTGATGATCTGCTGCTGCAAGAGTCTCGGCTCTG 962
Db 901 CTCATCATCTGCTCTACACCTGATGATCTGCTGCTGCAAGAGTCTCGGCTCTG 960
QY 963 TCTGGCTCCGAGAGAGAGCCGAAATCTCCGCGCATCACCAGCTGCTGCTGATGA 1022
Db 961 TCTGGCTCCGAGAGAGAGCCGAAATCTCCGCGCATCACCAGCTGCTGCTGATGA 1020
QY 1023 GTTCCAGTCTTCATCTGTGTGGACCCCAATTCACATCTTATCTGATGCTGCTG 1082
Db 1021 GTTCCAGTCTTCATCTGTGTGGACCCCAATTCACATCTTATCTGATGCTGCTG 1080
QY 1083 GGAAGCACTTCCACAGACAGCTGCGCTCTCCAGCTATTAATTTCTGATGCTGCTG 1142
Db 1081 GGAAGCACTTCCACAGACAGCTGCGCTCTCCAGCTATTAATTTCTGATGCTGCTG 1140
QY 1143 TATACCAACAGCAGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
Db 1141 TATACCAACAGCAGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1203 TGTATTAGGACTTCTGCTTCCCTATTAGATGGAATGGAGCGCCAGACCAATAGA 1262
Db 1201 TGTATTAGGACTTCTGCTTCCCTATTAGATGGAATGGAGCGCCAGACCAATAGA 1260
QY 1263 GTTAAACACAGCTTACAGATCTGCTTCCATGAGAGATGTGGAGGGATGAATAAGCCA 1322
Db 1261 GTTAAACACAGCTTACAGATCTGCTTCCATGAGAGATGTGGAGGGATGAATAAGCCA 1320
QY 1323 GTATGACTAGTGGAAATGTCTTCTTATTTCTCCAGGTAGAGAGATTCATATGAT 1382
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Db 1321 STATGACTAGTGGTAAATGCTTCTTATTGTTCTCCAGGTAGAGAGATTCATGAT 1380
QY 1383 CTTGGTTTAAACCCAGATTACACTGCAG 1410
Db 1381 CTTGGTTTAAACCCAGATTACACTGCAG 1408

RESULT 3
Q86725
ID Q86725 standard; cDNA; 2481 BP.
AC Q86725; 1995 (first entry)
DE Mammalian kappa opioid receptor protein cDNA.
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
OS amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
Rattus rattus.
FH Key Location/Qualifiers
FT cds l11..1253
FT /product= kappa opioid receptor
FT /tag= a
PN J07070191-A.
PD 14-MAR-1995.
PF 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 95-144857/19.
DR P-PSDB; R72591.
DR Kappa opioid receptor protein and cells expressing it - useful
PT for the screening of compounds for analgesic and hypnotic
PS properties
PS Claim 2: Page 9-10; 15pp; Japanese.
CC The nucleotide sequence of the novel mammalian kappa opioid receptor
CC cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA
CC by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC the mouse delta-opioid receptor gene. This fragment was cloned into the
CC plasmid pRIT to produce pRIT1. The plasmid pRIT1 was used to probe a rat
CC brain DNA library in lambda ZAPII to obtain a clone of the rat kappa
CC opioid receptor gene, designated pKOPR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SQ Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T;

Query Match 8.9%; Score 125; DB 1; Length 2481;
Best Local Similarity 98.9%; Pred. No. 1.le-52;
Matches 275; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 576 TCGAAGATGTTCATTTCATTGACTACTACACATGTTTACACATATTCACCTTGACC 635
Db 501 TCGAAGATGTTCATTTCATTGACTACTACACATGTTTACACATATTCACCTTGACC 630
QY 636 ATGATGATGTGGACCGCTACCTGTGTGCCACCTGTGAAAGCTTTGGACTTCCGA 695
Db 561 ATGATGATGTGGACCGCTACCTGTGTGCCACCTGTGAAAGCTTTGGACTTCCGA 620
QY 696 ACACCTTTGAAAGCAAGATCATCATCTGATTTGGCTTCTGCAATCATCTGTTGT 755
Db 621 ACACCTTTGAAAGCAAGATCATCATCTGATTTGGCTTCTGCAATCATCTGTTGT 680
QY 756 ATATACGATAGTCTCTTGGAGGCACCAAGTCAGGAGATGTGGATGATGATGATG 815
Db 681 ATATACGATAGTCTCTTGGAGGCACCAAGTCAGGAGATGTGGATGATGATGATG 740
QY 816 TCCTTCGATTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 853
Db 741 TCCTTCGATTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 778

RESULT 4
T92601
ID T92601 standard; cDNA; 1275 BP.
```

576 TGCAAGATTGTCATTTCCATTGACTACTACAACATGTTTACCAGCATATTCACCTTGACC

```

Query Match          5.5%; Score 77; DB 1; Length 12/5;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 77; Conservative 0; Mismatches 0; Indels 0; caps 0;

```

FT WO9601898-A1. /note= "incomplete termination codon"
 PN 25-JAN-1996.
 PD 07-JUL-1995; F00912
 PE 11-JUL-1994; FR-008531.
 PA (UYSI-) UNIV PASTEUR STRASBOURG LOUIS.
 PI Kieffer B, Simonin F;
 PR WPI; 96-097628/10.
 DR P-PSDB: R88722.
 DT New nucleic acid encoding the human kappa opioid receptor - useful
 PT in diagnosis and therapy, and for isolating receptor ligands and
 PT modulators
 PS Claim 3; Page 13-15; 30pp; French.
 CC This sequence codes for the human kappa opioid receptor and was
 CC obtained from two overlapping cDNA fragments isolated from a
 CC human placental cDNA library. The fragments were amplified from
 CC the library using PCR primers based on the sequence of human
 CC genomic clones which hybridised with a murine delta receptor cDNA
 CC probe. Nucleotide probes derived from the kappa opioid receptor
 CC coding sequence are useful for diagnosis of neurological, cardio-
 CC vascular and psychiatric disorders associated with opioid
 CC receptors.
 SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;
 0;

Query Match 2.3%; Score 32; DB 1; Length 1142;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TACATATTAACTGGCTTTGGCAGATGCTTT 505
 DB 289 TACATATTAACTGGCTTTGGCAGATGCTTT 320
 |||||

RESULT 7
 T90998
 ID T90998 standard; cDNA; 1143 BP.
 AC T90998;
 DT 14-APR-1998 (first entry)
 DE Human kappa opioid receptor cDNA.
 KW Selective target cell activation; G protein-coupled receptor;
 KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;
 KW human; transgenic animal; arrhythmia; bone disease; seizure;
 KW vascular contraction; disease model; ss.
 OS Homo sapiens.
 PN WO9735478-A1.
 PD 02-OCT-1997.
 PF 25-MAR-1997; U05334.
 PR (REGC) UNIV CALIFORNIA.
 PA Conklin BR;
 DR WPI; 97-502739/46.
 DT P-PSDB: W30297.
 PT Selective activation of target cell expressing modified G protein
 PT coupled receptor - allows control of cellular proliferation,
 PT especially for amplification of transfected cells in gene therapy
 PS Example 1; Page 74-76; 117pp; English.
 CC This cDNA sequence comprises the coding region for human kappa
 CC opioid receptor (KOR, see W30297), a G protein-coupled receptor
 CC implicated in neurotransmission. A novel method for selectively
 CC activating a target cell (TC) comprises: (i) introducing into the
 CC cell a nucleic acid sequence (I) that expresses a G protein-coupled
 CC receptor (A) modified to be activated superiorly by a synthetic
 CC ligand (RASSL); and (ii) exposing the transfected cell to small
 CC synthetic molecules (B) that bind to and activate (A), inducing the
 CC activation. Coupled cellular response associated with receptor
 CC activation. (A) has: (a) decreased binding affinity for a selected
 CC natural ligand of the native receptor; (b) binding affinity for
 CC (B); and (c) is activated by binding (B) sufficiently to produce
 CC the required cellular response. Also new are: (1) transgenic cells
 CC including heterologous (I) in the genome; (2) cellular implants
 CC comprising a TC transfected with (I); (3) isolated (I); and (4)
 CC transgenic non-human animals expressing (A). Activation of (A)

CC results, in vitro or in vivo, in cellular proliferation, or
 CC secretion of a cellular product, particularly a heterologous
 CC therapeutic protein encoded by a second inserted nucleic acid
 CC sequence. Particularly it is used to expand the relatively few
 CC cells that are successfully transfected during gene therapy
 CC procedures. Other responses that can be regulated are cell
 CC migration and contraction, or pigment production. In transgenic
 CC animals, expression or stimulation of (A) is designed to develop
 CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
 CC contractions, dementia, neurodegeneration etc., for use as models
 CC of these diseases (claimed). The transgenic animals are also used
 CC for production of improved food products (e.g. increased calcium
 CC content in eggshells or altered fat/lean ratios) or to control
 CC fertility or induce labour. A RASSL derived from KOR, designated
 CC RASSL ORI (see W30299), was generated by mutation of the KOR
 CC cDNA sequence.
 SQ Sequence 1143 BP; 237 A; 337 C; 283 G; 286 T;
 0;

Query Match 2.3%; Score 32; DB 1; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TACATATTAACTGGCTTTGGCAGATGCTTT 505
 DB 289 TACATATTAACTGGCTTTGGCAGATGCTTT 320
 |||||

RESULT 8
 T90999
 ID T90999 standard; cDNA; 1284 BP.
 AC T90999;
 DT 14-APR-1998 (first entry)
 DE Human kappa opioid receptor modified cDNA.
 KW Selective target cell activation; G protein-coupled receptor;
 KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;
 KW human; transgenic animal; arrhythmia; bone disease; seizure;
 KW vascular contraction; disease model; ss.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Synthetic.
 FH Key Location/Qualifiers
 FT sig_peptide 1..90 /*tag= a
 FT mat_peptide 91..1284 /*tag= b
 FT /*product= prolactin signal sequence
 FT /*product= FLAG-KOR-HA fusion
 PN WO9735478-A1.
 PD 02-OCT-1997.
 PF 25-MAR-1997; U05334.
 PR 26-MAR-1996; US-622348.
 PA (REGC) UNIV CALIFORNIA.
 PI Conklin BR;
 DR WPI; 97-502739/46.
 DT P-PSDB: W30298.
 PT Selective activation of target cell expressing modified G protein
 PT coupled receptor - allows control of cellular proliferation,
 PT especially for amplification of transfected cells in gene therapy
 PS Example 1; Page 77-79; 117pp; English.
 CC This cDNA sequence encodes a polypeptide (see W30298) comprising
 CC the human G protein-coupled kappa opioid receptor (KOR) (see also
 CC W30297) flanked by sequences that facilitate the detection and
 CC purification of recombinant KOR, and especially KOR RASSLS (see
 CC W30299), i.e. a receptor activated superiorly by a synthetic
 CC ligand. A novel method for selectively activating a target cell
 CC (TC) comprises: (i) introducing into the cell a nucleic acid
 CC sequence (I) that expresses a RASSL (A) and (ii) exposing the
 CC transfected cell to small synthetic molecules (B) that bind to and
 CC activate (A), inducing the G protein coupled cellular response
 CC associated with receptor activation. (A) has: (a) decreased binding
 CC affinity for a selected natural ligand of the native receptor; (b)
 CC binding affinity for (B); and (c) is activated by binding (B)
 CC sufficiently to produce the required cellular response. Also new

CC are: transgenic cells including heterologous (I) in the genome;
 CC cellular implants comprising a TC transfected with (I); isolated
 CC (I); and transgenic animals expressing (A). Activation of (A)
 CC results, in vitro or in vivo, in cellular proliferation, or
 CC secretion of a cellular product, particularly a heterologous
 CC therapeutic protein encoded by a second inserted nucleic acid
 CC sequence. Particularly it is used to expand the relatively few
 CC cells that are successfully transfected during gene therapy
 CC procedures. Other responses that can be regulated are cell
 CC migration and contraction, or pigment production. In transgenic
 CC animals, expression or stimulation of (A) is designed to develop
 CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
 CC contractions, dementia, neurodegeneration etc., for use as models
 CC of these diseases (claimed). The transgenic animals are also used
 CC for production of improved food products (e.g. increased calcium
 CC content in eggshells or altered fat/lean ratios) or to control
 CC fertility or induce labor.
 CC Sequence 1284 BP; 265 A; 377 C; 322 G; 320 T;
 SQ

Query Match 2.3%; Score 32; DB 1; Length 1284;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 TACATATTACCTGGCTTTGGCAGATGCTTT 505
 Db 400 TACATATTACCTGGCTTTGGCAGATGCTTT 431

RESULT 9
 Q56702
 ID Q56702 standard; DNA; 2447 BP.
 AC Q56702;
 DT 15-SEP-1994 (first entry)
 DE Partial sequence of the human kappa opioid receptor
 DE genomic clone H14 (XOR).
 KW Opioid receptor; morphine; opiate; ss.
 OS Homo sapiens.
 PN WO9404552-A.
 PD 03-MAR-1994.
 PE 13-AUG-1993; U07665.
 PR 13-AUG-1992; US-829200.
 FA (REGC.) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI; 94-083099/10.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT cpos. for opioid (antagonist) activity
 PT Example; Fig 8b; 74pp; English.
 CC To isolate opiate receptor genomic clones, 300,000 human genomic
 CC clones and a similar number of mouse genomic clones were probed
 CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 pst/XbaI
 CC fragment. One mouse clone and three human genomic clones were
 CC isolated. The 3 human clones had very different EcoRI patterns
 CC which indicated that three different genes were represented by the
 CC human genomic clones which were designated H3, H14 and H20. H14 maps
 CC to chromosome 8. It encodes the human kappa opioid receptor.
 CC Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;
 SQ

Query Match 2.2%; Score 31; DB 1; Length 2447;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 ATAGTCCTTGGAGGCCACCAAGTCAGGGAAG 795
 Db 213 ATAGTCCTTGGAGGCCACCAAGTCAGGGAAG 243

RESULT 10
 Q29156
 ID Q29156 standard; DNA; 822 BP.
 AC Q29156;

DT 08-MAR-1993 (first entry)
 DE Brain somatostatin receptor 5' DNA.
 KW SR; antibodies; tumours; glycoprotein; pancreatic somatostatinoma;
 KW rat; ss.
 OS Rattus rattus.
 FH Location/Qualifiers
 FT cds 1..822
 FT /*tag= a
 PN EP-508221-A.
 PD 14-OCT-1992.
 PE 25-MAR-1992; 105164.
 PR 28-MAR-1991; US-677009.
 PR 07-JAN-1992; US-817921.
 FA (AMCY) AMERICAN CYANAMID CO.
 PI Corbett MJ, Eppler CM, Haddock J, Hulmes JD, Shieh H;
 PI Srinad J, Zyskjr, Cecil ME;
 PI WPI; 92-341551/42.
 DR P-PSDB; R27505.
 DR New somatostatin receptor, active fragments and antibodies -
 PT prevents somatostatin binding to its receptor, useful for
 PT treating and detecting tumours e.g. pancreatic somatostatinoma
 PT Claim 18; Fig 10; 50pp; English.
 PS A partial clone of purified pituitary somatostatin was used to design
 CC PCR primers for amplification of somatostatin receptor DNA i.e.
 CC from the deduced location of the receptor cDNA was obid. This sequence
 CC ICII, a 501 bp fragment of the receptor cDNA was obid. This sequence
 CC was used in PCR to obtain the 5' rat brain SR sequence (some bases
 CC undefined and having a gap in the sequence). The receptor may be
 CC used to raise antibodies for detection and treatment of tumours in
 CC patients, and to treat e.g. pancreatic somatostatinoma, and to
 CC regulate the action of somatostatin in vivo.
 CC See also Q29154-7 and Q35865-6.
 CC Sequence 822 BP; 158 A; 245 C; 220 G; 194 T;
 SQ

Query Match 2.1%; Score 29; DB 1; Length 822;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 AAGATGAAGACCGCAACCAATCTACAT 478
 Db 262 AAGATGAAGACCGCAACCAATCTACAT 290

RESULT 11
 Q75928
 ID Q75928 standard; DNA; 1330 BP.
 AC Q75928;
 DT 17-AUG-1995 (first entry)
 DE Mouse opioid receptor-like receptor MOP2 cDNA.
 KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
 KW transmembrane domain; somatostatin; receptor; human; expression vector;
 KW truncate; chimaeric; assay; probe; ss.
 OS Mus musculus.
 FH Location/Qualifiers
 FT Key 161..1264
 FT cds /*tag= a
 FT /product= mouse opioid receptor-like receptor
 PN WO9428132-A.
 PD 08-DEC-1994.
 PE 20-MAY-1994; U05747.
 PR 20-MAY-1993; US-066296.
 PR 30-JUL-1993; US-100694.
 PR 05-NOV-1993; US-147592.
 PA (ARCH-) ARCH DEV CORP.
 PI Bell GI, Reisine I, Yasuda K;
 PI WPI; 95-022804/03.
 DR P-PSDB; R67671.
 DR Polynucleotides and peptides derived from opioid receptor
 PT polypeptides - for use in therapeutic compositions and in
 PT screening assays for useful drug substances.
 PS Claim 28; Page 225-229; 300pp; English.

CC The nucleotide sequence of the novel mouse opiod receptor-like receptor
 CC gene MOP2. MOP2 is a mouse receptor with pharmacological properties which
 CC are dissimilar to the properties of classic opiod receptors such kappa,
 CC delta, mu or sigma. It has been found that drug of high abuse potential
 CC or analgesic potency bind selectively to this receptor. This suggests
 CC that this receptor could be important in the development of drugs to
 CC treat addiction. Other opiod receptors isolated and produced such as the
 CC novel mouse kappa and delta opiod receptors (Q75926-7) are useful for
 CC the development of novel assays designed to select or improve substances,
 CC capable of interacting with the opiod receptor proteins, for use in
 CC diagnosis, drug design and therapeutic applications.
 CC Sequence 1330 BP; 250 A; 388 C; 350 G; 362 T;

Query Match 1.8%; Score 25; DB 1; Length 1330;

Best Local Similarity 100.0%; Pred. No. 0.0061;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACACATGTTTACCAGCA 621

|||||

Db 539 GACTACTACACATGTTTACCAGCA 563

RESULT 12

ID Q89233 standard; cDNA; 1567 BP.

AC Q89233;

DT 20-OCT-1995 (first entry)

DE Rat opiod receptor cDNA.

KW Opiod receptor; MOR-1; gene therapy; diagnostic; ss.

OS Rattus sp.

FT Key Location/Qualifiers

FT cds 173..1276

FT /*tag= a

PN WO9507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; U10358.

PR 13-SEP-1993; US-120601.

PA (INDV) UNIV INDIANA FOUND.

PI Yu L;

DR WPI: 95-131351/17.

DR P-PSDB; R71968.

PT New nucleic acid encoding new human mu opiod receptor - and

PT related vectors, transformed cells, antibodies etc., useful in

PT diagnosis, treatment and drug screening.

PS Example 9; Page 218-222; 266pp; English.

CC The cDNA given in Q89233 was isolated from a rat brain library by

CC low stringency hybridization with rat mu opiod receptor cDNA

CC (Q89222). The clone encoded a 367-amino acid protein (R71968)

CC that showed high homology with mu, kappa and delta opiod receptors

CC but lacked affinity for their ligands, suggesting it to be

CC a novel member of the opiod receptor family.

SQ Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T;

Query Match

Best Local Similarity 1.8%; Score 25; DB 1; Length 1567;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACACATGTTTACCAGCA 621

|||||

Db 551 GACTACTACACATGTTTACCAGCA 575

RESULT 13

ID Q90096 standard; cDNA; 2600 BP.

AC Q90096;

DT 03-NOV-1995 (first entry)

DE Mouse kappa-3 opiod receptor.

KW kappa-3 opiod receptor; analgesia; ss.

OS Mus sp.

FT Key Location/Qualifiers

FT cds

FT 299..1402

FT /*tag= a

PN WO9512616-A.

PD 11-MAY-1995.

PF 03-NOV-1994; U12728.

PR 05-NOV-1993; US-147949.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Pan Y, Pasternak GW;

DR WPI: 95-198814/25.

DR P-PSDB; R74298.

PT Nucleic acid molecule(s) encoding a kappa-3 opiod receptor, and

PT antibody against the receptor - used to detect the receptor, and to

PT image cell membrane-bound receptor in a subject

PS Disclosure; Fig.1; 68pp; English.

CC Degenerate primers based on conserved sequences of the mouse delta

CC opiod receptor were used in PCR to amplify mouse kappa-3 opiod

CC receptor cDNA from a mouse brain lambda ZAP cDNA library.

SQ Sequence 2600 BP; 536 A; 680 C; 663 G; 721 T;

Query Match

Best Local Similarity 1.8%; Score 25; DB 1; Length 2600;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACACATGTTTACCAGCA 621

|||||

Db 677 GACTACTACACATGTTTACCAGCA 701

RESULT 14

ID Q92972 standard; DNA; 2706 BP.

AC Q92972;

DT 22-DEC-1995 (first entry)

DE Rat opiorph receptor OR7 DNA.

KW Opiorph receptor; opiod; ss.

OS Rattus sp.

PN WO9519986-A1.

PD 27-JUL-1995.

PF 20-JAN-1995; U00939.

PR 21-JAN-1994; US-185360.

PA (AMCY) AMERICAN CYANAMID CO.

PI Eppler CM, Hulmes JD, Ozenberger BA;

DR WPI: 95-269412/35.

DR P-PSDB; R76638.

PT New isolated DNA encoding an opiorph receptor - used to develop

PT prods. for identifying opiod agonists and antagonists and for

PT detection and manipulation

PS Disclosure; Fig.1; 35pp; English.

CC Primers based on rodent opiod receptors were used to amplify rat

CC genomic DNA. Products were re-amplified and subcloned into pCR-II

CC vector and amplified in E. coli. Plasmid DNAs were isolated, and

CC an unspliced sequence was obt'd. (Q92972) encoding the transmembrane

CC domain opiorph receptor protein OR7.

SQ Sequence 2706 BP; 569 A; 675 C; 704 G; 758 T;

Query Match

Best Local Similarity 1.8%; Score 25; DB 1; Length 2706;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACACATGTTTACCAGCA 621

|||||

Db 485 GACTACTACACATGTTTACCAGCA 509

RESULT 15

T89585

ID T89585 standard; cDNA; 1452 BP.

AC T89585;

DT 12-JAN-1998 (first entry)

DE Rat orphanin FQ receptor cDNA clone LC132.

KW Orphanin FQ receptor; binding; locomotor disease; diagnosis;

KW treatment; opioid inhibitor; opiate induced hypothermia; drug design;
 OS morphine induced analgesia; methadone specific opioid receptor; ss.

EH Rattus sp.
 FT 5'UTR Location/Qualifiers
 Key 1..181
 FT /*tag= a
 CDS 182..1285
 FT /*tag= b
 FT 1286..1452
 FT 3'UTR
 FT /*tag= c

PN WO9707212-A1.
 PD 27-FEB-1997.
 PF 12-AUG-1996; U13305.
 PR 03-NOV-1995; US-553058.
 PR 11-AUG-1995; US-514451.
 PA (UWOR-) UNIV OREGON HEALTH SCI.
 PI Bunzow JR, Civeilli O, Grandy DK, Grisel JE, Mogil JS;
 PI Monsma FJ, Notack H-P, Reinscheid RK;
 PI WPI; 97-165296/15.
 DR P-PSDB; W25217.
 PT Mammalian orphanin FQ receptor inhibitor - used in the diagnosis and
 PT treatment of locomotor disease.
 PS Claim 5; page 42-43; 68pp; English.
 CC T89585 is rat orphanin FQ (OFQ) receptor cDNA clone LCL32. Highly
 CC specific peptides that bind the OFQ receptor were identified as
 CC OFQ receptor inhibitors. The peptides can be used to antagonise a
 CC physiological effect of an opioid in an animal. The peptides antagonise
 CC opiate induced hypothermia and morphine induced analgesia in animals.
 CC They may also be used in the diagnosis and treatment of locomotor
 CC disease. The peptides may also be used in the design of a methadone
 CC specific opioid receptor (MSOR); in drug design and for the isolation
 CC of endogenous receptors for anti-opioid agonists and antagonists found
 CC in plasma, serum, lymph, cerebrospinal fluid etc.
 SQ Sequence 1452 BP; 276 A; 414 C; 377 G; 385 T;

Query Match 1.8%; Score 25; DB 1; Length 1452;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTAGACAACTGTTACCAGCA 621

Db 560 GACTACTAGACAACTGTTACCAGCA 584

Search completed: February 17, 2000, 10:11:06
 Job time: 1921 sec

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OM nucleic - nucleic search, using sw model

Run on: February 17, 2000, 09:40:05 ; Search time 45.68 Seconds

(without alignments)
3695.460 Million cell updates/sec

Title: US-08-455-683-1

Perfect score: 1410

Sequence: 1 GGCACCTGCTGATCCCAA.....AACCCAGATTACAACTGCAG 1410

Scoring table: OLIGO_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA.*

Word size : 0

Number of hits that pass the threshold : 428588
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/PCU89_COMB.seq.*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	1.8	1452	1	US-08-149-093A-3
2	25	1.8	2600	2	US-08-147-949A-1
3	25	1.8	1452	3	US-08-911-245-3
4	25	1.8	1452	2	US-08-553-058C-3
5	25	1.8	1452	3	US-08-514-451A-3
6	25	1.8	2706	3	US-08-454-549-1
7	25	1.8	1567	6	PCI-US94-10358-16
8	23	1.6	1829	4	US-08-411-859-1
9	20	1.4	90	4	US-08-411-859-7
10	20	1.4	1618	6	PCI-US94-10358-1
11	20	1.4	1618	6	PCI-US94-10358-3
12	20	1.4	1610	6	PCI-US94-10358-7
13	17	1.2	1796	1	US-07-816-283-11
14	17	1.2	2061	1	US-08-204-656B-9
15	17	1.2	2061	1	US-08-470-702-5
16	17	1.2	2061	1	US-08-467-831-5
17	17	1.2	10564	1	US-08-206-176-5
18	17	1.2	1796	2	US-08-417-103-11
19	17	1.2	11725	3	US-08-756-508-1
20	17	1.2	1498	4	US-08-775-428-1
21	17	1.2	1324	4	US-08-330-272-1
22	17	1.2	1324	6	PCI-US95-13663-1
23	16	1.1	1352	1	US-07-714-819-1
24	16	1.1	7350	1	US-07-865-662F-14
25	16	1.1	186	1	US-08-222-177A-12
26	16	1.1	1352	1	US-08-246-978A-1
27	16	1.1	1731	1	US-08-203-905B-13
28	16	1.1	3066	1	US-08-142-439A-1
29	16	1.1	1909	1	US-08-142-439A-3
30	16	1.1	3243	2	US-08-369-798-3
31	16	1.1	2607	2	US-08-369-798-5
32	16	1.1	5437	2	US-08-416-872-1

33	16	1.1	1352	2	US-08-440-814A-1	Sequence 1, Appli
34	16	1.1	2141	2	US-08-463-931-1	Sequence 1, Appli
35	16	1.1	819	2	US-08-792-019B-4	Sequence 4, Appli
36	16	1.1	2254	2	US-08-153-848-27	Sequence 27, Appli
37	16	1.1	1500	2	US-08-443-568B-15	Sequence 15, Appli
38	16	1.1	1711	2	US-08-749-903-2	Sequence 2, Appli
39	16	1.1	1875	2	US-08-453-956-14	Sequence 14, Appli
40	16	1.1	1875	2	US-08-086-631-14	Sequence 14, Appli
41	16	1.1	885	2	US-08-411-706-3	Sequence 3, Appli
42	16	1.1	1870	2	US-08-592-126-86	Sequence 86, Appli
43	16	1.1	3066	3	US-08-869-477-1	Sequence 1, Appli
44	16	1.1	1909	3	US-08-869-477-3	Sequence 3, Appli
45	16	1.1	522	7	5391485-3	Patent No. 5391485

ALIGNMENTS

RESULT 1
US-08-149-093A-3
; Sequence 3, Application US/08149093A
; Patent No. 5658783
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K
; TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific
; TITLE OF INVENTION: Opioid Receptor Gene and Uses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banter & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,093A
FILING DATE: 06-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5658783han, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..181
FEATURE:
NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-08-149-093A-3

Query Match 1.8%; Score 25; DB 1; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACACATGTTTACCAGCA 621
|||||
Db 560 GACTACTACACATGTTTACCAGCA 584

RESULT 2
US-08-147-949A-1
; Sequence 1, Application US/08147949A
; Patent No. 5747279
; GENERAL INFORMATION:
; APPLICANT: Pasternak, Gavril W.
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTORS
; TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,949A
; FILING DATE: 05-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44782/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 423523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEtical: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 299..1401
; OTHER INFORMATION:
; US-08-147-949A-1

Query Match 1.8%; Score 25; DB 2; Length 2600;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACACATGTTTACCAGCA 621
|||||
Db 677 GACTACTACACATGTTTACCAGCA 701

RESULT 3
US-08-911-245-3
; Sequence 3, Application US/08911245
; Patent No. 5821067
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K

; TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
; TITLE OF INVENTION: Opioid Receptor Gene and Uses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,245
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149093
; FILING DATE: 06-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5821067nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
; US-08-911-245-3

Query Match 1.8%; Score 25; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 GACTACTACACATGTTTACCAGCA 621
|||||
Db 560 GACTACTACACATGTTTACCAGCA 584

RESULT 4
US-08-553-058C-3
; Sequence 3, Application US/08553058C
; Patent No. 5821219
; GENERAL INFORMATION:
; APPLICANT: Grisel, Judith E.
; APPLICANT: Grandy, David K.
; APPLICANT: Mogil, Jeffrey S.
; TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon

```

; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Version WP6, ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,058C
; FILING DATE: 11/3/95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5821219nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-40006/WDN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: CDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
; US-08-553-058C-3

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Query Match 1.8%; Score 25; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 597 GACTACTACACATGTTTACCAGCA 621
|||||
Db 560 GACTACTACACATGTTTACCAGCA 584

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RESULT 5
US-08-514-451A-3
; Sequence 3, Application US/08514451A
; Patent No. 5837809
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R.
; APPLICANT: Grandy, David K.
; APPLICANT: Civelili, Olivier
; APPLICANT: Reinscheid, Rainer K.
; APPLICANT: No. 5837809hacker, Hans-Peter
; APPLICANT: Monsma, Frederick J.
; TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WP5.1 ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,451A
; FILING DATE: 08/11/95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/553,058
; FILING DATE: 11/13/95
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5837809nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-45995/WDN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: CDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..181
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 182..1282
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1283..1452
; US-08-514-451A-3

```

```

Query Match 1.8%; Score 25; DB 3; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 597 GACTACTACACATGTTTACCAGCA 621
|||||
Db 560 GACTACTACACATGTTTACCAGCA 584

```

```

RESULT 6
US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5868324
; GENERAL INFORMATION:
; APPLICANT: EPPLER, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HULMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995

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Query Match	1.8%; Score 25; DB 3; Length 2706;	Best Local Similarity	100.0%; Pred. No. 0.0034;	Mismatches	0; Indels	0; Gaps
QY	597 GACTACTACACATGTTTACCAGCA 621					
DB	485 GACTACTACACATGTTTACCAGCA 509					
<p>CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Robinson, Joseph R. REGISTRATION NUMBER: 33,448 REFERENCE/DOCKET NUMBER: 0646/1A818-US5 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 527-7700 TELEFAX: (212) 753-6237 TELEX: 236687 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2706 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE: TISSUE TYPE: Rat brain US-08-454-549-1</p>						
<p>Query Match 1.8%; Score 25; DB 3; Length 2706; Best Local Similarity 100.0%; Pred. No. 0.0034; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>						
QY	597 GACTACTACACATGTTTACCAGCA 621					
DB	485 GACTACTACACATGTTTACCAGCA 509					
<p>RESULT 7 PCT-US94-10358-16 ; Sequence 16, Application PC/TUS9410358 ; GENERAL INFORMATION: ; APPLICANT: ; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS ; NUMBER OF SEQUENCES: 17 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Arnold, White & Durkee ; STREET: P. O. Box 4433 ; CITY: Houston ; STATE: Texas ; COUNTRY: USA ; ZIP: 77210 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII ; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25 ; CURRENT APPLICATION NUMBER: PCT/US94/10358 ; FILING DATE: Concurrently herewith ; CLASSIFICATION: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/120,601 ; FILING DATE: 13 SEPTEMBER 1993 ; ATTORNEY/AGENT INFORMATION: ; NAME: WILSON, MARK B. ; REGISTRATION NUMBER: 37,259 ; REFERENCE/DOCKET NUMBER: INDA005P-- ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (512) 418-3000 ; TELEFAX: (713) 789-2679 ; TELEX: 79-0924 ; INFORMATION FOR SEQ ID NO: 16: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 1567 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: cDNA ; NAME/KEY: CDS</p>						
<p>Query Match 1.8%; Score 23; DB 4; Length 1829; Best Local Similarity 100.0%; Pred. No. 0.0033; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>						
QY	591 TCCATTGACTACTACACATGTT 613					
DB	404 TCCATTGACTACTACACATGTT 426					
<p>CLASSIFICATION: 173...1273 PCT-US94-10358-16 ; LOCATION: 173...1273 ; Query Match 1.8%; Score 25; DB 6; Length 1567; ; Best Local Similarity 100.0%; Pred. No. 0.0034; ; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>						
QY	597 GACTACTACACATGTTTACCAGCA 621					
DB	551 GACTACTACACATGTTTACCAGCA 575					
<p>RESULT 8 US-08-411-859-1 ; Sequence 1, Application US/08411859 ; Patent No. 5985600 ; GENERAL INFORMATION: ; APPLICANT: EVANS, CHRISTOPHER J. ; APPLICANT: KEITH JR., DUANE E. ; APPLICANT: EDWARDS, ROBERT H. ; TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID ; TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED ; TITLE OF INVENTION: PHARMACEUTICALS ; NUMBER OF SEQUENCES: 15 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Morrison & Foerster ; STREET: 755 Page Mill Road ; CITY: Palo Alto ; STATE: California ; COUNTRY: USA ; ZIP: 94304-1018 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/411,859 ; FILING DATE: ; CLASSIFICATION: 424 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/929,200 ; FILING DATE: 13-AUG-1992 ; ATTORNEY/AGENT INFORMATION: ; NAME: LATHGOW, TIMOTHY J. ; REGISTRATION NUMBER: 36,856 ; REFERENCE/DOCKET NUMBER: 22000-20526.00 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 415-813-5600 ; TELEFAX: 415-494-0792 ; TELEX: 706141 ; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 1829 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; FEATURE: ; NAME/KEY: CDS ; LOCATION: 29..1144 ; US-08-411-859-1</p>						

```
RESULT 9
US-08-411-859-7
; Sequence 7, Application US/08411859
; Patent No. 5985600
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH JR., DUANE E.
; APPLICANT: EDWARDS, ROBERT H.
; TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
; TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411.859
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/929,200
; FILING DATE: 13-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: LITHGOW, TIMOTHY J.
; REGISTRATION NUMBER: 36,856
; REFERENCE/DOCKET NUMBER: 22000-20526.00
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-411-859-7

Query Match 1.4%; Score 20; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 TTCTGGTGAAGAACTTCAA 1198
Db 58 TTCTGGTGAAGAACTTCAA 77

RESULT 10
PCT-US94-10358-1
; Sequence 1, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
; PCT-US94-10358-1

Query Match 1.4%; Score 20; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 GTGGACCGCTACATGCTGT 664
Db 700 GTGGACCGCTACATGCTGT 719

RESULT 11
PCT-US94-10358-3
; Sequence 3, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
```

```
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 339..1235
PCT-US94-10358-3

Query Match 1.4%; Score 20; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 GTGACGCTACATTGCTGT 664
| | | | | | | | | | | | | | | |
Db 700 GTGACGCTACATTGCTGT 719

RESULT 12
PCT-US94-10358-7
; Sequence 7, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/120,601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
PCT-US94-10358-7

Query Match 1.4%; Score 20; DB 6; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 TTTCGGATGAAACTTCAA 1198
| | | | | | | | | | | | | | | |
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Db 1256 TTTCGGATGAAACTTCAA 1275

RESULT 13
US-07-816-283-11
; Sequence 11, Application US/07816283
; Patent No. 5438155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1796 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-816-283-11

Query Match 1.2%; Score 17; DB 1; Length 1796;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 ATGAGTGTGGACCGCTA 655
| | | | | | | | | | | | | | | |
Db 565 ATGAGTGTGGACCGCTA 581

RESULT 14
US-08-204-656B-9
; Sequence 9, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuo
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
```



```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Library of chromosomal DNA from Bacillus
; LIBRARY: macerans, pMAC, generated by treating chromosomal DNA from Bacillus mac
; LIBRARY: IAM1243 with a restriction enzyme, and inserting and linking restrictive
; LIBRARY: fragments to pBR322
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2061
; OTHER INFORMATION: /note= "Nucleotides 1-2061
; OTHER INFORMATION: correspond to nucleotides 82-2142 of the Bacillus macerans
; OTHER INFORMATION: cyclomaltodextrin glucanotransferase structural gene"
;
; US-08-204-656B-9
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Query Match 1.2%; Score 17; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ACGGTGACTTGGGAAGG 146
|||||
Db 1978 ACGGTGACTTGGGAAGG 1994

```
RESULT 15
US-08-470-702-5
; Sequence 5, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
; US-08-470-702-5
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Query Match 1.2%; Score 17; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ACGGTGACTTGGGAAGG 146
|||||
Db 1978 ACGGTGACTTGGGAAGG 1994

Search completed: February 17, 2000, 10:11:58
Job time: 1913 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2000, 09:37:05 ; Search time 771.69 Seconds
(without alignments)
6898.737 Million cell updates/sec

Title: US-08-455-683-1
Perfect score: 1410
Sequence: 1 GGCACCTCTGATGCCAA.....AACCCAGATTACAACTGCAG 1410
Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST *

Word size : 0

Number of hits that pass the threshold : 9077268

- 1: em_est1:*
- 2: em_est2:*
- 3: em_est3:*
- 4: em_est4:*
- 5: em_est5:*
- 6: em_est6:*
- 7: em_est7:*
- 8: em_est8:*
- 9: em_est9:*
- 10: em_est10:*
- 11: em_est11:*
- 12: em_est12:*
- 13: em_est13:*
- 14: em_est14:*
- 15: em_est15:*
- 16: em_est16:*
- 17: em_est17:*
- 18: em_est18:*
- 19: em_est19:*
- 20: gb_est1:*
- 21: gb_est2:*
- 22: gb_est3:*
- 23: gb_est4:*
- 24: gb_est5:*
- 25: gb_est6:*
- 26: gb_est7:*
- 27: gb_est8:*
- 28: gb_est9:*
- 29: gb_est10:*
- 30: gb_est11:*
- 31: gb_est12:*
- 32: gb_est13:*
- 33: gb_est14:*
- 34: gb_est15:*
- 35: gb_est16:*
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- 37: gb_est18:*
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59: gb_est33:*

60: gb_est34:*

61: gb_est35:*

62: gb_est36:*

63: gb_est37:*

64: gb_est38:*

65: em_est27:*

66: em_est28:*

67: em_est29:*

68: em_est30:*

69: gb_est39:*

70: gb_est40:*

71: gb_est41:*

72: gb_est42:*

73: gb_est43:*

74: gb_est44:*

75: em_est31:*

76: em_est32:*

77: em_est33:*

78: em_est34:*

79: gb_gss1:*

80: gb_gss2:*

81: gb_gss3:*

82: gb_gss4:*

83: em_gss1:*

84: em_gss2:*

85: em_gss3:*

86: em_gss4:*

87: gb_gss5:*

88: gb_gss6:*

89: gb_gss7:*

90: gb_gss8:*

91: gb_gss9:*

92: em_gss5:*

93: em_gss6:*

94: em_gss7:*

95: em_gss8:*

96: em_gss9:*

97: em_gss10:*

98: em_gss11:*

99: gb_gss10:*

100: gb_gss11:*

101: em_gss12:*

102: gb_gss12:*

103: gb_gss13:*

104: gb_gss14:*

105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	1.8	153	22	R31984
C 2	22	1.6	427	64	AW047705
3	20	1.4	303	37	AA683100
4	20	1.4	401	64	AL120154
5	20	1.4	601	74	AV387715
C 6	20	1.4	509	74	AW200827
C 7	20	1.4	407	82	AQ674484
					R31984 yb2c10.r1
					AW047705 UI-M-BH1-
					AA683100 ae81g12.s
					AL120154 DKF26761A
					AV387715 AV387715
					AW200827 se9a02.y
					AQ674484 HS_5478_B

C	8	20	1.4	555	87	AQ810283	HS_4786_A
	9	19	1.3	398	41	AI009309	EST203760
	10	19	1.3	443	41	AI056367	OY48c06.x
	11	19	1.3	447	43	AI105468	EST214757
C	12	19	1.3	890	43	AI226332	u07406.y
	13	19	1.3	452	46	AI410541	EST238834
	14	19	1.3	559	46	AI410875	EST239169
	15	19	1.3	233	48	AI559367	tu21b12.x
	16	19	1.3	504	48	AI602174	UI-R-ABO-
	17	19	1.3	679	50	AI798222	tu66b12.x
	18	19	1.3	302	59	AI106245	AV106245
C	19	19	1.3	515	63	AI959497	fd10u03.y
	20	19	1.3	616	81	B72980	RPC1111-10M2
	21	19	1.3	657	82	AQ681658	HS_2161_A
	22	19	1.3	468	87	AQ807655	HS_3031_B
	23	19	1.3	161	103	AQ472185	CITBT-EI-
	24	19	1.3	394	103	AQ472191	CITBT-EI-
C	25	19	1.3	368	105	AQ424279	PC193-EC
	26	19	1.3	511	105	AQ661946	HS_2093_B
	27	18	1.3	352	21	R04688	PK27e08.r1
	28	18	1.3	433	23	H41020	yp72d11.s1
	29	18	1.3	384	25	N57941	YV61g04.s1
C	30	18	1.3	414	25	N62652	za14g10.s1
	31	18	1.3	448	25	N78731	zb05a11.s1
	32	18	1.3	429	25	W09072	mag3f06.r1
	33	18	1.3	349	27	AA000300	mg32a09.r
	34	18	1.3	374	28	C15712	C15712 Clon
	35	18	1.3	523	28	C15915	C15915 Clon
	36	18	1.3	651	29	AA130056	zn62e11.r
	37	18	1.3	680	29	AA196290	z929g04.s
C	38	18	1.3	466	30	AA218901	zq15e05.s
	39	18	1.3	206	31	AA317847	EST19840
	40	18	1.3	364	32	AA366615	EST77582
	41	18	1.3	477	33	AA407460	EST00811
	42	18	1.3	521	33	AA447244	zw93c04.r
	43	18	1.3	469	34	AA468769	ns09f02.s
C	44	18	1.3	580	35	AA565655	nk26g06.s
C	45	18	1.3	383	36	AA610438	np91g02.s

ALIGNMENTS

RESULT	1	R31984	153 bp	EST	28-APR-1995
LOCUS		Yh52c10.r1	Soares placenta Nb2HP Homo sapiens	cdna clone	
DEFINITION		IMAGE:134322.5	similar to gb:L25119 MU-TYPE OPIOID RECEPTOR (HUMAN);	mrna sequence.	
ACCESSION		R31984	1	GI:787827	
VERSION		R31984.1			
KEYWORDS		EST.			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS		Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.			
TITLE		The WashU-Merck EST Project			
JOURNAL		Unpublished (1995)			
COMMENT		Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 947 High quality sequence stops: 120 Source: IMAGE Consortium, LLNL			

FEATURES	source	location/qualifiers	1. 133	/organism="Homo sapiens"	
		/db_xref="GDB:540134"			
		/db_xref="taxon:9606"			
		/clone="IMAGE:134322"			
		/clone.lib="Soares placenta Nb2HP"			
		/sex="Female"			
		/dev_stage="placenta obtained at birth (full term)"			
		/lab_host="DH10B (ampicillin resistant)"			
		/note="Organ: placenta; Vector: pT73B (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cdna was primed with a Not I - oligo(dT) primer [5' AACTGGAGAGATTCGGCGCGAGGATTTTCTTTTCTTTT 3'1, double-stranded cdna was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "			
BASE COUNT	25 a	49 c	37 g	42 t	
ORIGIN					
Query Match	1.8%	Score 26;	DB 22;	Length 153;	
Best Local Similarity	100.0%;	Pred. No. 0.0035;			
Matches	26;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	915	GTCGCTACACCGTCGATGATCCGCG 940			
Db	45	GTCGCTACACCGTCGATGATCCGCG 70			
RESULT	2				
LOCUS	AW047705/c	427 bp	mrna	EST	18-SEP-1999
DEFINITION	UI-M-BH1-alo-f-04-0-UI.s1 NIH_BMAP_M_S2 Mus musculus				
	UI-M-BH1-alo-f-04-0-UI 3',				
	mrna sequence.				
ACCESSION	AW047705				
VERSION	AW047705.1	GI:5908234			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 427)				
AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.				
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery				
JOURNAL	Genome Res. 6 (9), 791-806 (1996)				
MEDLINE	97044477				
COMMENT	On Jun 22, 1998 this sequence version replaced gi:3245886.				
	Contact: Chib, H				
	National Institute of Mental Health				
	6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD				
	20892-9643, USA				
	Tel: 301 443 1706				
	Fax: 301 443 9890				
	Email: MEST@mail.nih.gov				
	The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cdna and therefore this may represent a bonafide poly A tail. The sequence tag present in the cdna between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cerebellum library cdna library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cdna clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cdna clones, this record will be updated accordingly when that means is determined.				

```

Seq primer: M13 Forward
POLYA=Yes.
FEATURES
  source
    1..427
      Location/Qualifiers
        /organism="Mus musculus"
        /db_xref="taxon:10090"
        /strain="C57BL/6J"
        /clone="UI-M-BH1-alo-f-04-0-UI"
        /clone_lib="NIH_BMAP_M_S2"
        /dev_stage="27-32 days"
        /lab_host="DHI0B (Life Technologies)"
        /note="Vector: pT73D-Pac (Pharmacia) with a modified
        polylinker; Site_1: Not I; Site_2: Eco RI; The
        NIH_BMAP_M_S2 library is a subtracted library derived from
        NIH_BMAP_M_S1, which in turn is a subtracted library
        derived from a mixture of normalized libraries from ten
        regions of the mouse brain (cerebellum, brain stems,
        olfactory bulbs, hypothalamus, cortex, amygdala, basal
        ganglia, pineal gland, striatum, hippocampus). The driver
        used for subtraction consisted of a pool of 5,000 clones
        from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
        obtained from non-normalized and normalized mouse brain
        spinal cord libraries.
        TAG_LIB=NIH_BMAP_M_S2
        TAG_TISSUE=cerebellum
        TAG_SEQ=GAGTC"
  BASE COUNT      119 a      104 c      107 g      97 t
  ORIGIN
    Query Match      1.6%; Score 22; DB 64; Length 427;
    Best Local Similarity 100.0%; Pred. No. 0.54;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 600 TACTACACATGTTTACCAGCA 621
      |||||||
  Db 355 TACTACACATGTTTACCAGCA 334

  RESULT 3
  AA683100 303 bp mRNA EST 15-DEC-1997
  LOCUS ae8lg12.s1 stratagene schizo brain s11 Homo sapiens cDNA clone
  DEFINITION IMAGE:970630 3', similar to SW:MAPA_RAT_P34926
  MICROTUBULE-ASSOCIATED PROTEIN 1A ; mRNA sequence.
  ACCESSION AA683100
  VERSION AA683100.1 GI:2658991
  KEYWORDS EST.
  SOURCE human.
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (bases 1 to 303)
  AUTHORS Hillier,D., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
    Krieman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
    Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
    Theising,B., White,Y., Wyllie,I., Waterston,R. and Wilson,R.
    WashU-NCI human EST Project
  TITLE Unpublished (1997)
  JOURNAL
  COMMENT On Sep 19, 1997 this sequence version replaced gi:1520424.
    Contact: Wilson RK
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    This clone is available royalty-free through LML ; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    Possible reversed clone: similarity on wrong strand
    Possible reversed clone: polyI not found
  Seq primer: -40m13 fwd. ET from Amersham
  High quality sequence stop: 229.
    Location/Qualifiers
  BASE COUNT      64 a      157 c      93 g      86 t      1 others
  ORIGIN

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    1..303
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:970630"
      /clone_lib="Stratagene schizo brain s11"
      /sex="male"
      /tissue_type="schizophrenic brain S-11 frontal lobe"
      /dev_stage="34 years old"
      /lab_host="SOLR (kanamycin resistant)"
      /note="Vector: Bluescript SK-; Site_1: EcoRI; Library
      constructed from S-11 frontal lobe, male, 34 years old,
      50% caucasian, 50% Aleutian. Schizophrenic suicide.
      Random primed into EcoRI site of ZAP II Vector. Mass
      excised. Custom library. Avg insert length 1.4kb.
      Material obtained by Johnston N., Torrey, E.F., Volken R.,
      and the Stanley Neuropathology Consortium - Analysis of
      RNAs from the Brains of Individuals with Psychiatric
      Diseases (Unpublished) Stanley Neurovirology Laboratory,
      Johns Hopkins School of Medicine, Baltimore MD."
      /base_count      51 a      118 c      68 g      66 t
  BASE COUNT
  ORIGIN

  Query Match      1.4%; Score 20; DB 37; Length 303;
  Best Local Similarity 100.0%; Pred. No. 6.8;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 1100 CACAGCTGCCCTCTCCAGCT 1119
      |||||||
  Db 113 CACAGCTGCCCTCTCCAGCT 132

  RESULT 4
  AL120154 401 bp mRNA EST 27-SEP-1999
  LOCUS DKFp761A137.rl 761 (synonym: hamy2) Homo sapiens cDNA clone
  DEFINITION DKFp761A137.5', mRNA sequence.
  ACCESSION AL120154
  VERSION AL120154.1 GI:5926053
  KEYWORDS EST.
  SOURCE human.
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (bases 1 to 401)
  AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
    EST (Koehrer, et al.)
    Unpublished (1999)
  JOURNAL
  COMMENT On Feb 18, 1999 this sequence version replaced gi:4297623.
    Contact: Koehrer K
    MIPS
    Am Klopferspitz 18a D-82152 Martinsried, Germany
    This is the 5' sequence of the clone insert
    Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
    Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
    sequenced by BMFZ within the cDNA sequencing consortium of the
    German Genome Project.
    No sl sequence available.
    This clone is available at the RZPD in Berlin.
    Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
    Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
    Location/Qualifiers
  BASE COUNT      64 a      157 c      93 g      86 t      1 others
  ORIGIN

```

REFERENCE
AUTHORS

Query Match 1.4%; Score 20; DB 64; Length 401;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 CACAGCTGCCCTCCAGCT 1119
|||||
Db 61 CACAGCTGCCCTCCAGCT 80

RESULT 5

AV387715 601 bp mRNA EST 09-DEC-1999
LOCUS AV387715 Chlamydomonas reinhardtii C9
DEFINITION cDNA clone CM028ell_r, mRNA sequence.

ACCESSION AV387715.1 GI:6541931

VERSION AV387715.1

KEYWORDS EST.

SOURCE Chlamydomonas reinhardtii.

ORGANISM Chlamydomonas reinhardtii.

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadaeae; Chlamydomonas.

1 (bases 1 to 601)

Asamizu,E., Nakamura,X., Sato,S., Fukuzawa,H. and Tabata,S.

A Large Scale Structural Analysis of cDNAs in a Unicellular Green

Alga, Chlamydomonas reinhardtii. I. Generation of 3451

non-redundant expressed sequence tags

DNA Res. (1999) In press

On Jul 6, 1999 this sequence version replaced gi:5422471.

Contact: Yasukazu Nakamura

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: ynakamura@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

source

1. 601 /organism="Chlamydomonas reinhardtii"

/strain="C9"

/db_xref="taxon:3055"

/clone="CM028ell_r"

/clone_lib="Chlamydomonas reinhardtii C9"

/dev_stage="photoautotrophic growth"

/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 138 a 171 c 165 g 127 t

ORIGIN

Query Match 1.4%; Score 20; DB 74; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 CAACATCTACATATTAC 486

|||||

Db 118 CAACATCTACATATTAC 137

RESULT 6

AW200827/c

LOCUS AW200827

DEFINITION se94a02.y1 Gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-cl027-387 5' similar to TR:Q9ZUS7 Q9ZUS7 F3G5.18 PROTEIN. ;

mRNA sequence.

ACCESSION AW200827.1 GI:5481556

VERSION AW200827

KEYWORDS EST.

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core

eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;

Glycine.

1 (bases 1 to 509)

Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,C.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

On Feb 18, 1999 this sequence version replaced gi:4299224.

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134 For further information

call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)

427-3324 or contact: clones@genomesystems.com or

info@genomesystems.com web site: www.genomesystems.com

High quality sequence stop: 406.

FEATURES

source

1. 509 /organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl027-387"

/clone_lib="Gm-cl027"

/tissue_type="cotyledons of 3- and 7-day-old Williams

seedlings"

/lab_host="DH10B"

/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated

from cotyledons of 3- and 7-day-old Williams seedlings

which were propagated on paper towels with distilled

water. The cotyledons were flash-frozen in liquid

nitrogen, then lyophilized for 72 hours. Unequal amounts

of mRNA was used for cDNA synthesis. Stratagene's cDNA

Synthesix Kit (catalog number 200401) was used to

synthesize the cDNA. First- stranded synthesis was

performed with 5-methyl dGTP, hence the ligated cDNA was

hemimethylated. A modification of Stratagene's

first-strand synthesis primer was used. An anchor

nucleotide (V=A, C, or G) was added to the 3' end of the

primer [GAGAGAGAGAGAGAGAGACTGCTGAG(T)18] to anchor

the primer at the 5' end of the poly(A) tract. After

second- strand synthesis, the cDNA ends were filled in

with cloned Pfu DNA, ligated to EcoRI adapters and

subsequently phosphorylated. The XhoI site within the

first-strand synthesis primer was then restricted by

digestion with XhoI; all XhoI sites in the cDNA would be

protected by their hemimethylated status. The cDNA

constructs were size-fractionated with a 500 bp cutoff,

using GibcoBRL Life Technologies' cDNA Size Fractionation

column. The column eluent was then ligated into

Stratagene's pBluescript(tm) II Xr Predigested vector

(pBluescript II SK(+)) that has been digested with EcoRI

and XhoI, and phosphorylated by Stratagene). 97% of the

white and blue colonies appear to contain recombinant

plasmids with cDNA inserts, based on size (n=30). This

library was constructed by Dr. Paul Keim and Dr. Virginia

Coryell."

BASE COUNT 139 a 138 c 96 g 135 t 1 others

ORIGIN

Query Match 1.4%; Score 20; DB 74; Length 509;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 TTCTGGCGCTTTGGAGATG 570

|||||

```

Db 229 TTCTTGGCCTTTGGAGATG 210

RESULT 7
AQ674484/c
LOCUS
DEFINITION
HS_5478_B2_G10.SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1054 Col=20 Row=N, genomic survey sequence.
ACCESSION
AQ674484
VERSION
AQ674484.1 GI:5207230
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 407)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 1054 row: N column: 20
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 407.
Location/Qualifiers
1. 407
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="Male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"

BASE COUNT 145 a 104 c 73 g 85 t
ORIGIN

FEATURES
source
1. 407
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="Male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"

Query Match 1.4%; Score 20; DB 82; Length 407;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 TGCTACTCTGTGGTATTG 396
|||||
Db 271 TGCTACTCTGTGGTATTG 252

RESULT 8
AQ810283/c
LOCUS
DEFINITION
HS_4786_AL_E12_17A CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=4786 Col=23 Row=I, genomic survey
sequence.
ACCESSION
AQ810283
VERSION
AQ810283.1 GI:5729525
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
1 (bases 1 to 396)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 4786 row: I column: 23
Seq primer: I7
Class: BAC ends
High quality sequence stop: 555.
Location/Qualifiers
1. 555
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="Male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT 190 a 137 c 98 g 128 t 2 others
ORIGIN

FEATURES
source
1. 555
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="Male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

Query Match 1.4%; Score 20; DB 87; Length 555;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 TGCTACTCTGTGGTATTG 396
|||||
Db 286 TGCTACTCTGTGGTATTG 267

RESULT 9
AI009309
LOCUS
DEFINITION
EST203760 Normalized rat heart, Bonto Soares Rattus sp. cDNA clone
EST.
ACCESSION
AI009309
VERSION
AI009309.1 GI:3223141
KEYWORDS
EST.
SOURCE
Rattus sp.
ORGANISM
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
1 (bases 1 to 396)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (Rat) Catalog & Rat
Gene Index
Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:2045441.
Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers

```

```

source
1. .338
/organism="Rattus sp."
/db_xref="ATCC (inhost):2020351"
/db_xref="taxon:10118"
/clone="RHEBL3"
/clone_lib="Normalized rat heart, Bento Soares"
/note="Organ: heart; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT      102 a      82 c      94 g      120 t
ORIGIN

Query Match      1.3%; Score 19; DB 41; Length 398;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCGTGTCATGTTTGTTCAT 436
|||||
Db 321 CTCGTGTCATGTTTGTTCAT 339

RESULT 10
LOCUS      AI056367      443 bp      mRNA      EST      24-SEP-1998
DEFINITION      oy48606.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669066 3',
mRNA sequence.
ACCESSION      AI056367
VERSION      AI056367.1 GI:3330233
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (Bases 1 to 443)
AUTHORS      NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
JOURNAL      Unpublished (1998)
COMMENT      On Sep 12, 1996 this sequence version replaced gi:1404573.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 593 Std Error: 0.00
Seq primer: -40ml3 fwd. EI from Amersham.
FEATURES
source
1. .443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1669066"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCGTACCAATCTGAGTGGGCGCGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      86 a      106 c      119 g      132 t

ORIGIN

Query Match      1.3%; Score 19; DB 41; Length 443;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 GGCACCAAGTCAGGGAAG 795
|||||
Db 152 GGCACCAAGTCAGGGAAG 170

RESULT 11
LOCUS      AI105468      447 bp      mRNA      EST      20-JAN-1999
DEFINITION      EST214757 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
RK18K82 3' end, mRNA sequence.
ACCESSION      AI105468
VERSION      AI105468.1 GI:3709542
KEYWORDS      EST.
SOURCE      Rattus sp.
ORGANISM      Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE      1 (Bases 1 to 447)
AUTHORS      Lee, N.H., Glodok, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
TITLE      Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
Gene Index
JOURNAL      Unpublished (1998)
COMMENT      Other_ESTs: TC53042
Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
FEATURES
source
1. .447
/organism="Rattus sp."
/db_xref="ATCC (inhost):2025917"
/db_xref="taxon:10118"
/clone="RK18K82"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT      122 a      85 c      99 g      141 t
ORIGIN

Query Match      1.3%; Score 19; DB 43; Length 447;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCGTGTCATGTTTGTTCAT 436
|||||
Db 424 CTCGTGTCATGTTTGTTCAT 442

RESULT 12
LOCUS      AI226352      890 bp      mRNA      EST      29-OCT-1998
DEFINITION      uf07a06.y1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
IMAGE:1510642 5', similar to SW:ARG2_MOUSE 008691 ARGINASE II
PRCURSOR ;, mRNA sequence.
ACCESSION      AI226352
VERSION      AI226352.1 GI:3809405
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

```


REFERENCE
AUTHORS
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 890)
Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Willson R. and Waterston R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2286647.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:937494
Seq primer: -40RP from Gibco
High quality sequence stop: 405.

FEATURES

source
1. 890
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1510642"
/clone_lib="Soares mouse mammary gland NLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 223 a 230 c 217 g 219 t 1 others
ORIGIN
Query Match 1.3%; Score 19; DB 43; Length 890;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 853 ATCTCTTCATGAGATCTG 871
|||||
Db 671 ATCTCTTCATGAGATCTG 653
RESULT 13
AI410541
LOCUS
DEFINITION
EST238834 Normalized rat heart, Bento Soares Rattus sp. cDNA clone
RHECY03 3' end, mRNA sequence.
ACCESSION
AI410541
VERSION
AI410541.1 GI:4254045
KEYWORDS
EST.
SOURCE
Rattus sp.
ORGANISM
Rattus sp.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 452)
Lee N.H., Glodek A., Chandra I., Mason T.M., Quackenbush J., Kerlavage A.R. and Adams M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
Unpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:3034510.
Contact: Lee, NH
ATCC

FEATURES
source
1. 452
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RHECY03"
/clone_lib="Normalized rat heart, Bento Soares"
/note="Organ: heart; Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 119 a 86 c 97 g 150 t
ORIGIN
Query Match 1.3%; Score 19; DB 46; Length 452;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCGTGTCATGTTGTCAI 436
|||||
Db 424 CTCGTGTCATGTTGTCAI 442
RESULT 14
AI410875
LOCUS
DEFINITION
EST239168 Normalized rat heart, Bento Soares Rattus sp. cDNA clone
RHECY48 3' end, mRNA sequence.
ACCESSION
AI410875
VERSION
AI410875.1 GI:4254379
KEYWORDS
EST.
SOURCE
Rattus sp.
ORGANISM
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 559)
Lee N.H., Glodek A., Chandra I., Mason T.M., Quackenbush J., Kerlavage A.R. and Adams M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
Unpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:3034844.
Contact: Lee, NH
ATCC

FEATURES
source
1. 559
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RHECY48"
/clone_lib="Normalized rat heart, Bento Soares"
/note="Organ: heart; Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 153 a 107 c 128 g 171 t
ORIGIN
Query Match 1.3%; Score 19; DB 46; Length 559;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 CTCGTGTCATGTTGTCAI 436
|||||
Db 424 CTCGTGTCATGTTGTCAI 442

```

RESULT 15
AI559367 233 bp mRNA EST 12-MAY-1999
LOCUS t21b12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168255 3',
DEFINITION mRNA sequence.
ACCESSION AI559367
VERSION AI559367.1 GI:4509572
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 233)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3189024.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldio, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 568 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 224
POLYA-No.

FEATURES             Location/Qualifiers
     source            1..233
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:2168255"
                        /tissue_type="anaplastic oligodendroglioma"
                        /lab_host="DH10B"
                        /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTGTTTTGTTTTGTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldio."
BASE COUNT          53 a 46 c 53 g 81 t
ORIGIN
Query Match          1.3%; Score 19; DB 48; Length 233;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 777 GGCACCAAGTCAGGGAAG 795
      |||||
Db 128 GGCACCAAGTCAGGGAAG 146

```

Search completed: February 17, 2000, 09:50:15
Job time: 790 sec

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Feb 17 11:11:36 2000; Maspar time 23.72 seconds
Tabular output not generated.
340.625 Million cell updates/sec

Title: >US-08-455-683-2
Description: (1-380) from US08455683.pep
Perfect Score: 2839
Sequence: 1 MESPIQIFRGDPGTCPSA.....RNTVQDPASMRDVGGMKPV 380
Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 35.005; Variance 158.855; scale 0.220

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2839	100.0	380	13	Mouse kappa opioid re	7.33e-252
2	2839	100.0	380	34	Mouse kappa opiate re	7.33e-252
3	2829	99.6	380	14	Rat kappa opiate rece	6.49e-251
4	2823	99.4	380	17	Mammalian kappa opioi	2.40e-250
5	2746	96.7	380	27	Human kappa opioid re	4.66e-243
6	2746	96.7	380	17	Human kappa opioid re	4.66e-243
7	2737	96.4	427	27	Human kappa opioid re	3.38e-242
8	2559	90.1	424	27	Human kappa opioid re	2.29e-225
9	2330	75.0	295	12	Human kappa opioid re	9.39e-185
10	1683	59.3	356	11	Murine mu-subtype opi	2.77e-142
11	1678	59.1	398	34	Mouse mu opiate recep	3.44e-142
12	1677	59.1	400	13	Human mu opiate recep	4.27e-142
13	1676	59.0	398	14	Rat mu opiate recep	6.58e-142
14	1674	59.0	398	13	Human mu opiate recep	5.30e-142
15	1675	59.0	400	14	Rat delta opiate rece	6.76e-136
16	1610	56.7	372	14	Rat delta opiate rece	6.76e-136

17	1597	56.3	372	9	R48629	Sequence of murine de
18	1597	56.3	372	13	R67670	Mouse delta opioid re
19	1597	56.3	372	34	W44938	Mouse delta opiate re
20	1499	52.8	371	10	R65503	Murine delta opioiid r
21	1473	51.9	367	13	R71968	Rat opioid receptor.
22	1471	51.8	367	13	R67671	Mouse opioid receptor
23	1464	51.6	367	14	R76638	Rat opiorph receptor
24	1444	50.9	367	25	W25882	Rat methadone-specifi
25	1444	50.9	367	36	W85549	Rat methadone-specifi
26	1444	50.9	367	24	W25217	Rat orphanin FQ recep
27	1195	42.1	367	13	R74298	Mouse kappa-3 opioiid
28	980	34.5	391	7	R39260	Murine somatostatin r
29	976	34.4	391	7	R39259	Human somatostatin re
30	922	32.5	369	7	R39262	Murine somatostatin r
31	912	32.1	369	7	R39261	Human somatostatin re
32	912	32.1	369	19	R97269	Human somatostatin re
33	901	31.7	369	5	R27504	Pituitary somatostati
34	850	29.9	333	13	R72985	Epsilon opioid recept
35	817	28.8	322	16	R48754	Rat RGH G-protein cou
36	817	28.8	322	19	W02726	Rat RGH G-protein c
37	815	28.7	418	7	R39263	Human somatostatin re
38	732	27.9	328	13	R72984	Epsilon opioid recept
39	732	25.8	428	7	R39264	Murine somatostatin r
40	679	23.9	242	23	W10017	G-protein coupled rec
41	623	21.9	355	25	W26588	Human MIP-1 alpha/RAN
42	623	21.9	355	11	R52749	C-C chemokine recepto
43	623	21.9	355	24	W25751	Human MIP-lalalpha/RAN
44	616	21.7	372	30	W52251	Rat galanin receptor
45	615	21.7	372	29	W40136	Rat GAIIR2 receptor pr

ALIGNMENTS

RESULT 1
ID R67669 standard; Protein; 380 AA.
AC R67669;

DT 17-AUG-1995 (first entry)
DE Mouse kappa opioid receptor MORK1.
KW Mouse: kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeraic; assay; probe.
OS Mus musculus.
PN W09428132-A.
PD 08-DEC-1994.
PE 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PI (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI: 95-022804/03.
DR NPSDB: Q75926.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 8; Page 207-211; 300pp; English.
CC The amino acid sequence of the novel mouse kappa opioid receptor MORK1.
CC The corresponding gene was isolated from a mouse brain cDNA library using
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRIF) receptor
CC subtypes SSR1, SSR2 and SSR3. The 1.2 kb PstI fragment from the mouse
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV
CC promoter-based expression vector pCMV-6b. The resultant construct
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete.
CC truncated or chimeraic opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 380 AA;

Query Match 100.0%; Score 2839; DB 13; Length 380;
Best Local Similarity 100.0%; Pred. No. 7.33e-252;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mespigifrgdgtcpsacillpnssswfnwaesdngsvsgedqglesahispaiv 60
QY 1 MESPIGIFRGDGTCPSPACILLPNSSSWFPNWAESDNGSVSGEDQGLESAHISPAIV 60
Db 61 itavysvfvglvgnslvnmfviirytkmktatniyifolaladalvtttmpfgsavyl 120
QY 1 MESPIGIFRGDGTCPSPACILLPNSSSWFPNWAESDNGSVSGEDQGLESAHISPAIV 60
Db 61 iitavysvfvglvgnslvnmfviirytkmktatniyifolaladalvtttmpfgsavyl 120
QY 1 IITAVYSVFPVGLVGNLSLVNMFVIIRYTKMKTATNIYIFNLALADALVTTFMPFGSAVYL 120
Db 121 mnswpfgdvclckvisidyymfmsiftlmmssvdyvavchpvykaldfrtpikakiini 180
QY 121 MNSWPFQDVCLCKVISIDYIYMFMSIFTLMMSSVDYVAVCHVPVKALDFRTPPLKAKIINI 180
Db 181 ciwllassvgisaivlggtkvredvdiacsldfpddehyswdlfnkicvfvfafvipvl 240
QY 181 CIWLLASSVGISAILVGGTKVREDVDVIECSLQFPDDEYSWDLFNKICVVFVFAVIPVL 240
Db 241 iivcvtlmliriksrvllsgsrekdrnlriiklvrvvavfiicwtphihilvealg 300
QY 241 IIVCVTLMILIRIKSRVLLSGSREKDRNLRIIKLVVVAVFIICWTPHIIHILVEALG 300
Db 301 stshstaalsyxfcialgtyntsslnpvlafidnkrfofrdfcpikmrmrgstnrv 360
QY 301 STSHSTAALSSYXFICIALGTYNTSSLPVLAFIDNKRFOFRDFCPIKMRMRGQSTNRV 360
Db 361 rntvgqpasmrdvggmnkpv 380
QY 361 RNTVQDPASMRDVGGMNKPV 380

RESULT 2
ID W44939 standard; Protein; 380 AA.
AC W44939;
DT 28-OCT-1998 (first entry)
DE Mouse kappa opiate receptor.
KW Mouse; Kappa opiate receptor; transgenic animal; mammal; identification;
KW exon; nervous tissue; pain; drug addiction; transplant rejection;
KW immunosuppressant; analgesic; morphine; side effect.
KW Mus sp.
OS Mus.
PN WO9802534-A2.
PD 22-JAN-1998.
PF 11-JUL-1997; F01282.
PR 15-JUL-1996; FR-006810.
PA (CNRS) CENT NAT RECH SCI.
PI Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin EH;
DR WPI; 98-110582/10.
DR N-PSDB; V49254.
PT Transgenic animals defective in one type of opioid receptor - used
PT to identify agents for treatment of pain, drug addiction and
PT transplant rejection, lacking side effects of known opiate(s)
PS Disclosure; Fig 13; 58pp; French.
CC This sequence represents the mouse kappa opiate receptor. The gene
CC sequence is used to generate a transgenic non-human mammal for
CC identifying agents for treating disorders associated with opiate
CC receptors. In the mammal, the expression of the gene encoding the
CC opiate receptor is modified, particularly by the deletion of an exon
CC and/or insertion of a marker gene, e.g. the neomycin resistance gene,
CC into the sequence. Especially the expression of the gene is altered
CC in nervous tissue. The agents are potentially useful for treating
CC severe pain (chronic or acute), drug addiction and/or prevention or
CC treatment of transplant rejection (as immunosuppressants). The method
CC may isolate and identify powerful analgesics that lack morphine-like
CC side effects.
SQ Sequence 380 AA;

Query Match 100.0%; Score 2839; DB 34; Length 380;
Best Local Similarity 100.0%; Pred. No. 7.33e-252;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mespigifrgdgtcpsacillpnssswfnwaesdngsvsgedqglesahispaiv 60

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Db 241 iivcytlmlrlksvllsgsrexdrnlrrtklrvvvavfiicwtppihifilvealg 300
QY 241 iivcytlmlrlksvllsgsrexdrnlrrtklrvvvavfiicwtppihifilvealg 300

Db 301 stshstavlssyfcialgytnsslnpvlvafldenfkrctfdcfpikmrmergstnr 360
QY 301 stshstavlssyfcialgytnsslnpvlvafldenfkrctfdcfpikmrmergstnr 360

Db 361 rntvdpasmdrvvgmknkv 380
QY 361 rntvdpasmdrvvgmknkv 380

RESULT 4
ID R72591 standard; Protein; 380 AA.
AC R72591;
DE Human kappa opioid receptor.
KW Mammalian kappa opioid receptor protein.
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
OS Rattus rattus.
FH Key Location/Qualifiers
FT cds 111..1253
FT /*tag= a
FT /product= kappa opioid receptor
PN J07070191-A.
PD 14-MAR-1995.
PF 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 95-144857/19.
DR N-PSDB; Q86725.
PI Kappa opioid receptor protein and cells expressing it - useful
PI for the screening of compounds for analgesic and hypnotic
PI properties
PS Claim 2; Page 9-10; 15pp; Japanese.
CC The amino acid sequence of the novel mammalian kappa opioid receptor.
CC The gene was isolated by amplifying a fragment from rat brain mRNA by
CC reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC the mouse delta-opioid receptor gene. This fragment was cloned into the
CC plasmid pCRII to produce pXII. The plasmid pXII was used to probe a rat
CC brain DNA library in lambda ZAP11 to obtain a clone of the rat kappa
CC opioid receptor gene, designated pKOPR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SQ Sequence 380 AA;

Query Match 99.4%; Score 2823; DB 14; Length 380;
Best Local Similarity 98.7%; Pred. No. 2.40e-250;
Matches 375; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1 mesqifgrgepgtccapsaclpnssswfnpwaesdngslgsedqglepahispalp 60
QY 1 MESQIFGRGDPGPTCCPSACLLPNSSSWFFNWAESDNGSVGSDQLESAAHISPALPV 60

Db 61 iitavysvfvvgvlvgsnlvmfviirytkmktatniyifnladalvttttmpfqsavyl 120
QY 61 IITAVYSVFFVVGVLVGSNLVMEFVIIRYTKMKTATNIYIFNLADALVTTTTPFQSAVYL 120

Db 121 mnswpfgdvclckivisidyymftsiftltmsvdryiavchpkykaldfrtptlkakiini 180
QY 121 MNSWPFGBDVCLCKIVISIDYNNFTSIFLTMSVDVRYIAVCHPVKALDFRTPLKAKIINI 180

Db 181 ciwllassvgisaivlgctkredvdiectslqfddpdeyswddlfmki cvfvafvipvl 240
QY 181 CIWLLASSVGISAIVLGCTKREDVDVIECTSLQFPDDEYSWDDLFMKICVFVAFVIPVL 240

Db 241 iivcytlmlrlksvllsgsrexdrnlrrtklrvvvavfiicwtppihifilvealg 300
QY 241 iivcytlmlrlksvllsgsrexdrnlrrtklrvvvavfiicwtppihifilvealg 300

Db 301 stshstavlssyfcialgytnsslnpvlvafldenfkrctfdcfpikmrmergstnr 360

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QY 301 STSHSTAALSSYFCIALGYTNSSLNPLVLYAFLDENFKRCDFCFPIKMRMERGSTNRV 360
Db 361 rntvdpasmdrvvgmknkv 380
QY 361 RNTVDPAASMDRVVGGMKNKV 380

RESULT 5
ID W30297 standard; Protein; 380 AA.
AC W30297;
DE Human kappa opioid receptor.
KW Selective target cell activation; G protein-coupled receptor;
KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;
KW human; transgenic animal; arrhythmia; bone disease; seizure;
KW vascular contraction; disease model.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 1..58
FT /label= N-terminus
FT /note= "extracellular"
FT 59..85
FT /label= TMH1
FT /note= "transmembrane"
FT 86..95
FT /label= I1
FT /note= "cytoplasmic"
FT 96..117
FT /label= TMH2
FT /note= "transmembrane"
FT 118..132
FT /label= E2
FT /note= "Extracellular"
FT 133..154
FT /label= TMH3
FT /note= "transmembrane"
FT 155..173
FT /label= I2
FT /note= "Cytoplasmic"
FT 174..196
FT /label= TMH4
FT /note= "transmembrane"
FT 197..222
FT /label= E2
FT /note= "extracellular"
FT 223..247
FT /label= TMH5
FT /note= "transmembrane"
FT 248..275
FT /label= I3
FT /note= "Cytoplasmic"
FT 276..299
FT /label= TMH6
FT /note= "Transmembrane"
FT 300..311
FT /label= E3
FT /note= "Extracellular"
FT 312..333
FT /label= TMH7
FT /note= "transmembrane"
FT 334..380
FT /label= C-terminus
FT /note= "cytoplasmic"
FT Disulfide_bond 131..210
FT Modified_site 25
FT /note= "potential N-glycosylation"
FT Modified_site 39
FT /note= "potential N-glycosylation"
FT Modified_site 345
FT /note= "palmitate"
PN W09735478-A1.
PD 02-OCT-1997.

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PF 25-MAR-1997; U05334.
 PR 26-MAR-1996; US-622348.
 PA (REGC) UNIV CALIFORNIA.
 PI Conklin BR;
 DR WPI: 97-502739/46.
 DR N-PSDB; 190998.
 PT Selective activation of target cell expressing modified G protein
 coupled receptor - allows control of cellular proliferation,
 especially for amplification of transfected cells in gene therapy
 Example 1: Page 74-76; 117pp; English.
 PS This protein comprises human kappa opioid receptor (KOR), a
 G protein-coupled receptor implicated in neurotransmission. A
 novel method for selectively activating a target cell (IC)
 comprises: (i) introducing into the cell a nucleic acid sequence
 (I) that expresses a G protein-coupled receptor (A) modified to be
 activated supercilously by a synthetic ligand (RASSL); and (ii)
 exposing the transfected cell to small synthetic molecules (B) that
 bind to and activate (A), inducing the G protein coupled cellular
 response associated with receptor activation. (A) has: (a)
 decreased binding affinity for a selected natural ligand of the
 native receptor; (b) binding affinity for (B); and (c) is activated
 by binding (B) sufficiently to produce the required cellular
 response. Also new are: (i) transgenic cells including
 heterologous (I) in the genome; (2) cellular implants comprising a
 IC transfected with (I); (3) isolated (I); and (4) transgenic
 non-human animals expressing (A). Activation of (A) results, in
 vitro or in vivo, in cellular proliferation, or secretion of a
 cellular product, particularly a heterologous therapeutic protein
 it is used by a second inserted nucleic acid sequence. Particularly
 it is used to expand the relatively few cells that are successfully
 transfected during gene therapy procedures. Other responses that
 can be regulated are cell migration and contraction, or pigment
 production. In transgenic animals, expression or stimulation of
 (A) is designed to develop cardiac arrhythmia, symptoms of bone
 disease, seizures, vascular contractions, dementia, neurodegeneration
 etc., for use as models of these diseases (claimed). The transgenic
 animals are also used for production of improved food products
 (e.g. increased calcium content in eggshells or altered fat/lean
 ratios) or to control fertility or induce labour. A RASSL derived
 from KOR, designated RASSL ORI (see W30299), was generated by
 mutation of the KOR cDNA sequence (see T90998).
 SQ Sequence 380 AA;

Query Match 96.7%; Score 2746; DB 27; Length 380;
 Best Local Similarity 93.7%; Pred. No. 4.66e-243;
 Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

Db 1 mdsqifrgpgptcapsacilppssawfpgwaepdsgsagsdaqlpahispaipv 60
 QY 1 MESPTQIFRGDGPCTCSPSACILPNSSSWFPNWAESDSNGSVGSEDDQLESASHISPAIPV 60

Db 61 iitavysvfvvlgynslvmfviirytkmktatniyifnladalavttmpfgstvy 120
 QY 61 IITAVYSVVVVGVLGNSLVMEFVIIRYTKMKTATNIYIFNLADALAVTTMPFGSAVYL 120

Db 121 mnswpfgdvlckivisidymnftsiftltmmsvdrlyavchpvcaldfrtclkakiini 180
 QY 121 MNSWFGDVLCKIVISIDYNNFTSIFTLTMMSVDRYIAVCHPVKALDFRTCLKAKIINI 180

Db 181 ciwllssvgsaisvlggtkvrddviesclqfpdddysswdlfnkicvfiavfipvl 240
 QY 181 CIWLLASSVGSIAVLGGTKVRDDVIECSLQFPDDDYSSWDLFMKICVFIAVFIPVL 240

Db 241 iivcyttmlrlksvrlslgsrekdrnlrritrlvllvvavfvvcwtpihifilvealg 300
 QY 241 IIVCYTTLMLRLKSVRLSLGSREKDRNLRITRLVLLVAVVAVFICWTPIHIFILVEALG 300

Db 301 stshstaalssyfcialgytnsslnpilyafldcnkrcfdrcfplkmmergstsv 360
 QY 301 STSHSTAALSSYFCIALGYTNSSLPVLYAFLDENKRCFRDRCFPIKMRERGSTNRV 360

Db 361 rntvqdpaylrdidgmknkv 380
 QY 361 RNTVQDPASMRDVGGMKNKPV 380

QY 361 RNTVQDPASMRDVGGMKNKPV 380

RESULT 6
 ID R88722 standard; Protein; 380 AA.
 AC R88722;
 DT 04-SEP-1996 (first entry)
 DE Human kappa opioid receptor.
 KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
 OS neurology; diagnosis.
 PN Homo sapiens.
 PN WO9601898-A1.
 PD 25-JAN-1996.
 PD 07-JUL-1995; F00912.
 PR 11-JUL-1994; FR-008531.
 PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
 PI Kieffer B, Simonin F;
 DR WPI: 96-097628/10.
 DR N-PSDB; T12550.
 PT New nucleic acid encoding the human kappa opioid receptor - useful
 in diagnosis and therapy, and for isolating receptor ligands and
 PT modulators
 PS Claim 7; Page 13-15; 30pp; French.
 CC The sequence coding for the human kappa opioid receptor was
 obtained from two overlapping cDNA fragments isolated from a
 human placental cDNA library. The fragments were amplified from
 the library using PCR primers based on the sequence of human
 genomic clones which hybridised with a murine delta receptor cDNA
 probe. Nucleotide probes derived from the kappa opioid receptor
 coding sequence are useful for diagnosis of neurological, cardio-
 vascular and psychiatric disorders associated with opioid
 receptors. The receptor can be used for identifying e.g. agonists
 of its activity for potential use as analgesics.
 SQ Sequence 380 AA;

Query Match 96.7%; Score 2746; DB 17; Length 380;
 Best Local Similarity 93.7%; Pred. No. 4.66e-243;
 Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

Db 1 mdsqifrgpgptcapsacilppssawfpgwaepdsgsagsdaqlpahispaipv 60
 QY 1 MESPTQIFRGDGPCTCSPSACILPNSSSWFPNWAESDSNGSVGSEDDQLESASHISPAIPV 60

Db 61 iitavysvfvvlgynslvmfviirytkmktatniyifnladalavttmpfgstvy 120
 QY 61 IITAVYSVVVVGVLGNSLVMEFVIIRYTKMKTATNIYIFNLADALAVTTMPFGSAVYL 120

Db 121 mnswpfgdvlckivisidymnftsiftltmmsvdrlyavchpvcaldfrtclkakiini 180
 QY 121 MNSWFGDVLCKIVISIDYNNFTSIFTLTMMSVDRYIAVCHPVKALDFRTCLKAKIINI 180

Db 181 ciwllssvgsaisvlggtkvrddviesclqfpdddysswdlfnkicvfiavfipvl 240
 QY 181 CIWLLASSVGSIAVLGGTKVRDDVIECSLQFPDDDYSSWDLFMKICVFIAVFIPVL 240

Db 241 iivcyttmlrlksvrlslgsrekdrnlrritrlvllvvavfvvcwtpihifilvealg 300
 QY 241 IIVCYTTLMLRLKSVRLSLGSREKDRNLRITRLVLLVAVVAVFICWTPIHIFILVEALG 300

Db 301 stshstaalssyfcialgytnsslnpilyafldcnkrcfdrcfplkmmergstsv 360
 QY 301 STSHSTAALSSYFCIALGYTNSSLPVLYAFLDENKRCFRDRCFPIKMRERGSTNRV 360

Db 361 rntvqdpaylrdidgmknkv 380
 QY 361 RNTVQDPASMRDVGGMKNKPV 380

RESULT 7
 ID W30298 standard; Protein; 427 AA.
 AC W30298;
 DT 14-APR-1998 (first entry)
 DE Human kappa opioid receptor fusion polypeptide.


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RESULT 8
ID W30299 standard; Protein; 424 AA.
AC W30299;
DI 14-APR-1998 (first entry)
DE Human kappa opioid receptor RASSL ORI.
KW Selective target cell activation; G protein-coupled receptor;
KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;
KW human; transgenic animal; arrhythmia; bone disease; seizure;
KW vascular contraction; disease model.
OS Chimeric - Homo sapiens.
FH Chimeric - Synthetic.
FT Key Location/Qualifiers
FT Peptide 1..30
FT /label= Sig_peptide
FT /note= "prolactin signal sequence"
FT Peptide 31..38
FT /label= FLAG
FT Protein 39..414
FT /label= KOR
FT /note= "human kappa opioid receptor"
FT Domain 39..95
FT /label= N-terminus
FT /note= "extracellular"
FT Domain 96..122
FT /label= TMH1
FT /note= "transmembrane"
FT Domain 123..132
FT /label= I1
FT /note= "cytoplasmic"
FT Domain 133..154
FT /label= TMH2
FT /note= "transmembrane"
FT Domain 155..169
FT /label= E2
FT /note= "Extracellular"
FT Domain 170..191
FT /label= TMH3
FT /note= "transmembrane"
FT Domain 192..210
FT /label= I2
FT /note= "Cytoplasmic"
FT Domain 211..233
FT /label= TMH4
FT /note= "transmembrane"
FT Domain 234..259
FT /label= E2
FT /note= "extracellular, contains 17 amino acid
FT residues from delta opioid receptor
FT (Val-235, Gln-237, Pro-238, Asp-240,
FT Gly-241, Ala-242, Val-243, Val-244,
FT Thr-246, Ser-251, Pro-252, Ser-253,
FT Trp-254, Tyr-255, Thr-258, Val-259,
FT Thr-260)"
FT Domain 260..281
FT /label= TMH5
FT /note= "transmembrane"
FT Domain 282..309
FT /label= I3
FT /note= "Cytoplasmic"
FT Domain 310..333
FT /label= TMH6
FT /note= "transmembrane"
FT Domain 334..345
FT /label= E3
FT /note= "Extracellular"
FT Domain 346..367
FT /label= TMH7
FT /note= "transmembrane"
FT Domain 368..414
FT /label= C-terminus
FT /note= "cytoplasmic"
FT Disulfide_bond 168..245

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FT Modified_site 62 /note= "potential N-glycosylation"
FT Modified_site 76 /note= "potential N-glycosylation"
FT Modified_site 382 /note= "palmitate"
FT Peptide 415..424 /label= HA
PN WO9735478-A1.
PD 02-OCT-1997.
PF 25-MAR-1997; U05334.
PR 26-MAR-1996; US-622348.
PA (REGC ) UNIV CALIFORNIA.
PI Conklin BR;
DR WPI; 97-502739/46.
DR N-PSDB; T92601.
PT Selective activation of target cell expressing modified G protein
PT coupled receptor - allows control of cellular proliferation,
PT especially for amplification of transfected cells in gene therapy
PT Example 1; Page 80-82; 11pp; English.
PS This protein comprises RASSL ORI, a G protein-coupled receptor that
CC is activated superiorly by synthetic ligands. ORI comprises human
CC G protein-coupled kappa opioid receptor (KOR) (see also W30297)
CC modified at 17 amino acid positions to contain the corresponding
CC amino acid of the delta opioid receptor, and containing N- and
CC C-terminal flanking sequences that facilitate the detection and
CC purification of recombinant protein. A novel method for selectively
CC activating a target cell (TC) comprises: (i) introducing into the
CC cell a nucleic acid sequence (I) (see T92601) that expresses a RASSL
CC (A) and (ii) exposing the transfected cell to small synthetic molecules
CC (B) that bind to and activate (A), inducing the G protein coupled
CC cellular response associated with receptor activation. (A) has (a)
CC decreased binding affinity for a selected natural ligand of the
CC native receptor; (b) binding affinity for (B); and (c) is activated
CC by binding (B) sufficiently to produce the required cellular response.
CC Also new are: transgenic cells including heterologous (I) in the
CC genome; cellular implants comprising a TC transfected with (I);
CC isolated (I); and transgenic animals expressing (A). Activation of
CC (A) results, in vitro or in vivo, in cellular proliferation, or
CC secretion of a cellular product, particularly a heterologous
CC therapeutic protein encoded by a second inserted nucleic acid
CC sequence. Particularly it is used to expand the relatively few
CC cells that are successfully transfected during gene therapy
CC procedures. Other responses that can be regulated are cell
CC migration and contraction, or pigment production. In transgenic
CC animals, expression or stimulation of (A) is designed to develop
CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC contractions, dementia, neurodegeneration etc., for use as models
CC of these diseases (claimed). The transgenic animals are also used
CC for production of improved food products (e.g. increased calcium
CC content in eggshells or altered fat/lean ratios) or to control
CC fertility or induce labour.
SQ Sequence 424 AA;
Query Match 90.1%; Score 2659; DB 27; Length 424;
Best Local Similarity 89.2%; Pred. No. 2,29e-225;
Matches 340; Conservative 20; Mismatches 16; Indels 5; Gaps 4;
Db 38 vdsplqifrgpgptcacsacplpnssawfpgwaepdngsagsedaglepahispaipv 97
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Qy 1 MESPIQIFRGDPGPTCSPSACLLPNSSWFPNWAESDSNGSVGSEDOLESASHIPAIPV 60
Db 98 itatvysvfvvgvlvgnslyvmfviirytkmtatniyifnaladalvtttmpfstvyl 157
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Qy 61 IITAVISVVFVVGVLGNSLVMEVIIRYTKMTATNIYIFNLALADALVTTMPFSAYYL 120
Db 158 moswpgdvlckivisidgvyymftsfilttmmsvdyiaavchpvaldfirtpkakiini 217
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Qy 121 MNSWPGDVLCKIVISIDYINNMFTSIFILTMMSVDYRIAVCHPVKALDFRPLPKAKINI 180
Db 218 ciwllassvgisaiylgvtqprdga-vv-ctllqbsp--swywdtvtkicvfifavipv 273
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 CIWLLASSVGISAIYLGSTKVEDVDVTECSLQFPDDEYSW-WDLFMKICVFAFVPIV 239

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[illegible]

MPRELH

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Feb 17 11:14:24 2000; MasPar time 8.92 seconds
Tabular output not generated. 552.170 Million cell updates/sec

Title: >US-08-455-683-2
Description: (1-380) from US08455683.pep
Perfect Score: 2839
Sequence: 1 MESPTQIFRGDPGPCPSA.....RNTVDPASMRDVGGMKPV 380

Scoring table: PAM 150
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 32.927; Variance 157.770; scale 0.209

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2826	99.5	380	1	US-08-149- Sequence 7, Applicatio	3.11e-238
2	2826	99.5	380	2	US-08-911- Sequence 7, Applicatio	3.11e-238
3	2685	94.6	378	2	US-08-514- Sequence 10, Applicati	1.39e-225
4	1887	66.5	330	2	US-08-454- Sequence 5, Applicatio	3.75e-154
5	1677	59.1	400	3	PCT-US94-1 Sequence 8, Applicatio	2.03e-135
6	1676	59.0	391	2	US-08-454- Sequence 3, Applicatio	2.50e-135
7	1674	59.0	398	3	PCT-US94-1 Sequence 2, Applicatio	3.76e-135
8	1674	59.0	398	1	US-08-149- Sequence 5, Applicatio	3.76e-135
9	1674	59.0	398	2	US-08-911- Sequence 5, Applicatio	3.76e-135
10	1610	56.7	367	2	US-08-454- Sequence 4, Applicatio	1.89e-129
11	1598	56.3	372	2	US-08-411- Sequence 2, Applicatio	2.22e-128
12	1597	56.3	372	2	US-08-411- Sequence 10, Applicati	2.72e-128
13	1593	56.1	372	2	US-08-911- Sequence 6, Applicatio	6.18e-128
14	1593	56.1	372	1	US-08-149- Sequence 6, Applicatio	6.18e-128
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18	1473	51.9	367	2	US-08-454- Sequence 2, Applicatio	2.94e-117
19	1444	50.9	367	1	US-08-149- Sequence 4, Applicatio	1.11e-114
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21	1444	50.9	367	2	US-08-514- Sequence 4, Applicatio	1.11e-114
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29	976	34.4	391	1	US-07-816- Sequence 2, Applicatio	2.95e-73
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32	922	32.5	369	1	US-08-417- Sequence 8, Applicatio	1.66e-68
33	912	32.1	369	1	US-08-417- Sequence 16, Applicati	1.26e-67
34	912	32.1	369	1	US-08-417- Sequence 6, Applicatio	1.26e-67
35	912	32.1	369	1	US-07-816- Sequence 6, Applicatio	1.26e-67
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ALIGNMENTS

RESULT 1
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Sequence 7, Application US/08149093A

Sequence 7, Application US/08149093A
Patent No. 5658783

GENERAL INFORMATION:

APPLICANT: Bunzov, James R

APPLICANT: Grandy, David K

TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific

TITLE OF INVENTION: Opioid Receptor Gene and Uses

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSER: Baner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,093A

FILING DATE: 06-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5658783nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,311

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

CC CC
CC NAME/KEY: Protein
CC LOCATION: 1..380
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
CC
SQ SEQUENCE 380 AA; 42652 MW; 802929 CN;

Query Match 99.5%; Score 2826; DB 1; Length 380;
Best Local Similarity 99.5%; Pred. No. 3.11e-238;
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MESPIQIFRGDPGPTCPSACLLPNSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60
QY 1 MESPIQIFRGDPGPTCPSACLLPNSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60

Db 61 IITAVYSVFWVGLVGNLSVMFVIIRYTKMTATNIYFNALADALVTTTTPQSAVYL 120
QY 61 IITAVYSVFWVGLVGNLSVMFVIIRYTKMTATNIYFNALADALVTTTTPQSAVYL 120

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AC xxxxxx
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CC Sequence 7, Application US/08911245
CC Patent No. 5821067
CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R
CC APPLICANT: Grandy, David K
CC TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
CC TITLE OF INVENTION: Opioid Receptor Gene and Uses
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Banner & Allegretti, Ltd.
CC STREET: 10 South Wacker Drive, Suite 3000
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/911,245
CC FILING DATE: 15-AUG-1997
CC CLASSIFICATION: 536

CC CC
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/149093
CC FILING DATE: 06-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5821067nan, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,311
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-715-1000
CC TELEFAX: 312-715-1234
CC TELEX: 910-221-5317
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 380 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..380
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
CC
SQ SEQUENCE 380 AA; 42652 MW; 802929 CN;

Query Match 99.5%; Score 2826; DB 2; Length 380;
Best Local Similarity 99.5%; Pred. No. 3.11e-238;
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 MESPIQIFRGDPGPTCPSACLLPNSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60
QY 1 MESPIQIFRGDPGPTCPSACLLPNSWFPNWAESDNGSVGSEDQQLSAHISPAIPV 60

Db 61 IITAVYSVFWVGLVGNLSVMFVIIRYTKMTATNIYFNALADALVTTTTPQSAVYL 120
QY 61 IITAVYSVFWVGLVGNLSVMFVIIRYTKMTATNIYFNALADALVTTTTPQSAVYL 120

Db 121 MNSWPFQGVLCIKVISIDYNNMFTSIITLTMMSVDRIAVCHPVKALDFRPLKAKIINI 180
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Db 181 CIWLLASSVGISAIVLGGTKVREDVDVTECSLQFPDDEYSWMDLFMKICVFAFVPIPVL 240
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVTECSLQFPDDEYSWMDLFMKICVFAFVPIPVL 240

Db 241 IIVCYITMILRLKSVLLSGSREKDRNLRIITKLVLVWVAVFIICWTPHIHIFILVEALG 300
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Db 301 STSHSTAALSSYYFCALGYTNSSLNPNVLYAFLDENKRCRDFCFPIKMERQSTNRV 360
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Db 361 RNTVQDPASMRDVGGMKNKP 380
QY 361 RNTVQDPASMRDVGGMKNKP 380

RESULT 3
ID US-08-514-451A-10 STANDARD; PRT; 378 AA.
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AC xxxxxx
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CC Sequence 10, Application US/08514451A
CC Patent No. 5837809
CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R.
CC APPLICANT: Grandy, David K.
CC APPLICANT: Civelli, Olivier
CC APPLICANT: Reinscheid, Rainer K.

CC APPLICANT: No. 5837809hacker, Hans-Peter
CC APPLICANT: Monsma, Frederick J.
CC TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
CC TITLE OF INVENTION: RECEPTOR LIGAND AND USES
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Klariquist Sparkman Campbell
CC ADDRESSEE: Leigh & Whinston LLP
CC STREET: 121 S.W. Salmon, Suite 1600
CC CITY: Portland
CC STATE: Oregon
CC COUNTRY: USA
CC ZIP: 97204

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy Disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WP5.1 ASCII text
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/514.451A
CC FILING DATE: 08/11/95
CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/553,058
CC FILING DATE: 11/13/95

CC ATTORNEY/AGENT INFORMATION:
CC NAME: William D. No. 5837809nan, M.D.
CC REGISTRATION NUMBER: 30,878
CC REFERENCE/DOCKET NUMBER: 899-45995/WDN
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (503) 226-7391
CC TELEFAX: (503) 228-9446

CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 378 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear

CC MOLECULE TYPE:
CC DESCRIPTION: peptide
CC SEQUENCE 378 AA; 42392 MW; 806199 CN;

Query Match 94.6%; Score 2685; DB 2; Length 378;
Best Local Similarity 96.6%; Pred. No. 1.39e-225;
Matches 367; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

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Db 61 IITAVYSVFWVGLVGNLSVFMFVIIRYTKMTATNIYIFNLALADALVTTMPFQSAVYL 120
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Db 239 IIVCYTILMLRLKSVRLSGSKKDRNLRLITKLVLVVAVFIICNTPIHIFILVEALG 298
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Sequence 5, Application US/08454549
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CC Sequence 5, Application US/08454549
CC Patent No. 5866324
CC GENERAL INFORMATION:
CC APPLICANT: EPPLER, C. Mark
CC APPLICANT: OZENBERGER, Bradley A.
CC APPLICANT: HULMES, Jeffrey D.
CC TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
CC TITLE OF INVENTION: TO OPIOID RECEPTORS
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Darby & Darby, P.C.
CC STREET: 805 Third Avenue
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/454,549
CC FILING DATE: 30-MAY-1995
CC CLASSIFICATION: 435

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robinson, Joseph R.
CC REGISTRATION NUMBER: 33,448
CC REFERENCE/DOCKET NUMBER: 0646/1A818-US5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 527-7700
CC TELEFAX: (212) 753-6237
CC TELEX: 236687

CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 330 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: Rat

CC SEQUENCE 330 AA; 36851 MW; 611728 CN;

Query Match 66.5%; Score 1887; DB 2; Length 330;
Best Local Similarity 85.8%; Pred. No. 3.75e-154;
Matches 326; Conservative 3; Mismatches 1; Indels 50; Gaps 1;

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QY 1 MESPIQIFRGDPGPTCPSACLLPNSSWFPNWAESDSNGSVGSEDQQLSAHISPAIPV 60
Db 61 IITAVYSVFWVGLVGNLSVFMFVIIRYTKMTATNIYIFNLALADALVTTMPFQSAVYL 120
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Db 121 MNSWFGDVLCKIVISIDYNNMFTSIFLTMTMSVDRIYAVCHPVKALDFRTPKAKIWI 136
QY 121 MNSWFGDVLCKIVISIDYNNMFTSIFLTMTMSVDRIYAVCHPVKALDFRTPKAKIWI 180
Db 137 -----SSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWMDLFMKICVVFVFAFVPIVL 190
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWMDLFMKICVVFVFAFVPIVL 240

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RESULT 7
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Sequence 2, Application PC/TUS9410358
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Sequence 2, Application PC/TUS9410358
XX
XX GENERAL INFORMATION:
XX
XX APPLICANT:
XX
XX TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
XX
XX NUMBER OF SEQUENCES: 17
XX
XX CORRESPONDENCE ADDRESS:
XX
XX ADDRESSEE: Arnold, White & Durkee
XX
XX STREET: P. O. Box 4433
XX
XX CITY: Houston
XX
XX STATE: Texas
XX
XX COUNTRY: USA
XX
XX ZIP: 77210
XX
XX COMPUTER READABLE FORM:
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XX MEDIUM TYPE: Floppy disk
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XX COMPUTER: IBM PC compatible
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XX OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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XX SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
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XX APPLICATION NUMBER: PCT/US94/10358
XX
XX FILING DATE: Concurrently herewith
XX
XX CLASSIFICATION:
XX
XX PRIOR APPLICATION DATA:
XX
XX APPLICATION NUMBER: 08/120,601
XX
XX FILING DATE: 13 SEPTEMBER 1993
XX
XX ATTORNEY/AGENT INFORMATION:
XX
XX NAME: WILSON, MARK B.
XX
XX REGISTRATION NUMBER: 37,259
XX
XX REFERENCE/DOCKET NUMBER: INDA005P--
XX
XX TELECOMMUNICATION INFORMATION:
XX
XX TELEPHONE: (512) 418-3000
XX
XX TELEFAX: (713) 789-2679
XX
XX TELEX: 79-0924
XX
XX INFORMATION FOR SEQ ID NO: 2:
XX
XX SEQUENCE CHARACTERISTICS:
XX
XX LENGTH: 398 amino acids
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XX TYPE: amino acid

CC CC TELEX: 910-221-5317

CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 398 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC FEATURE:

CC NAME/KEY: Protein

CC LOCATION: 1..398

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CC OTHER INFORMATION: /note= "Rat Mu-Opioid Receptor"

CC SEQUENCE 398 AA; 44508 MW; 870781 CN;

Query Match 59.0%; Score 1674; DB 1; Length 398;

Best Local Similarity 65.8%; Pred. No. 3.76e-135;

Matches 208; Conservative 54; Mismatches 50; Indels 4; Gaps 4;

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Db 128 YLMGTWPGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVKALDFTPRNAKIV 187

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Db 188 NVCNWLSSAIGLPVFMFATTKYRQG-S-IDCTLFSHPT-YWENLLKICVFIFAFIMP 244

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Db 365 RVRQNTREHPSTANTV 380

QY 359 RVR-NTVQDPASMRDV 373

RESULT 9

ID US-08-911-245-5 STANDARD; PRI; 398 AA.

XX xxxxxx

Sequence 5, Application US/08911245

Sequence 5, Application US/08911245

Patent No. 5821067

GENERAL INFORMATION:

APPLICANT: Bunzow, James R

APPLICANT: Grandy, David K

TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific

TITLE OF INVENTION: Opioid Receptor Gene and Uses

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CC CC APPLICATION NUMBER: US/08/911,245

CC FILING DATE: 15-AUG-1997

CC CLASSIFICATION: 536

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/149093

CC FILING DATE: 06-NOV-1993

CC ATTORNEY/AGENT INFORMATION:

CC NAME: No. 5821067nan, Kevin E

CC REGISTRATION NUMBER: 35,303

CC REFERENCE/DOCKET NUMBER: 93,311

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 312-715-1000

CC TELEFAX: 312-715-1234

CC TELEX: 910-221-5317

CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 398 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC FEATURE:

CC NAME/KEY: Protein

CC LOCATION: 1..398

CC OTHER INFORMATION: /label= Identifier

CC OTHER INFORMATION: /note= "Rat Mu-Opioid Receptor"

CC SEQUENCE 398 AA; 44508 MW; 870781 CN;

Query Match 59.0%; Score 1674; DB 2; Length 398;

Best Local Similarity 65.8%; Pred. No. 3.76e-135;

Matches 208; Conservative 54; Mismatches 50; Indels 4; Gaps 4;

Db 68 ATTIMALSYVCGVGLFGNFMVYVIRYTKMTATNIYIFNLADALATSTLPQSVN 127

QY 59 PVITAVYSVVFVGLVGNLSVNFVIRYTKMTATNIYIFNLADALVITTFPQSAV 118

Db 128 YLMGTWPGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVKALDFTPRNAKIV 187

QY 119 YLMNSWPGDVLCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVKALDFTPLKAKII 178

Db 188 NVCNWLSSAIGLPVFMFATTKYRQG-S-IDCTLFSHPT-YWENLLKICVFIFAFIMP 244

QY 179 NICIWLASSVGSIAVLGGIKVREDVDIECSLOFPDDEYSWDLFMKICVFVFAFVFP 238

Db 245 ILIITVCYGLMLRLKSVRLSSGSKDRNLRIIRFMVLVYVAVFVCHVTPHIVVILKA 304

QY 239 VLIITVCYTLMLRLKSVRLSSGSKDRNLRIIRFMVLVYVAVFVCHVTPHIFILVEA 298

Db 305 LITIPETTFQTVSWHFCIALGYNSCLNPVLYAFDENKRCFRFCIPTSTIEQNST 364

QY 299 LGSTSHSTAALSSYVFCIALGYNSCLNPVLYAFDENKRCFRFCIPTSTIEQNST 358

Db 365 RVRQNTREHPSTANTV 380

QY 359 RVR-NTVQDPASMRDV 373

RESULT 10

ID US-08-454-549-4 STANDARD; PRI; 367 AA.

XX xxxxxx

Sequence 4, Application US/08454549

Sequence 4, Application US/08454549

Patent No. 5866324

GENERAL INFORMATION:

APPLICANT: EPLER, C. Mark

APPLICANT: OZENERGER, Bradley A.

APPLICANT: HULMES, Jeffrey D.

TITLE OF INVENTION: CDNA's ENCODING PROTEINS CLOSELY RELATED

TITLE OF INVENTION: TO OPIOID RECEPTORS

CC NUMBER OF SEQUENCES: 13
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Darby & Darby, P.C.
 CC STREET: 805 Third Avenue
 CC CITY: New York
 CC STATE: New York
 CC COUNTRY: USA
 CC ZIP: 10022
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/454,549
 CC FILING DATE: 30-MAY-1995
 CC CLASSIFICATION: 435
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Robinson, Joseph R.
 CC REGISTRATION NUMBER: 33,448
 CC REFERENCE/DOCKET NUMBER: 0646/1A818-US5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (212) 527-7700
 CC TELEFAX: (212) 753-6237
 CC TELEX: 236687
 CC INFORMATION FOR SEQ ID NO: 4:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 367 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: not relevant
 CC TOPOLOGY: not relevant
 CC MOLECULE TYPE: protein
 CC ORIGINAL SOURCE:
 CC ORGANISM: Rat
 CC SEQUENCE 367 AA; 40122 MW; 712609 CN;
 Query Match 56.7%; Score 1610; DB 2; Length 367;
 Best Local Similarity 65.6%; Pred. No. 1,89e-129;
 Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;
 Db 15 LLANVDTFPAFASANAGSGPGR--SAS-SIALAIAITALYSAYCAVGLLGNVLWM 71
 QY 22 LLPNSSWFPNWAESDSNGSVGSEDOQLESAPAIPIITAVYSVVVGLVNSLWM 81
 Db 72 FGIVRYTKLTATNIYIFNLALADALATSTLPFQSAKYLMETWPEGLLCKAVLSIDYN 131
 QY 82 FVIRYTKATATNIYIFNLALADALVTTTPFQSAVYLMNSWPFQGLCKIVISIDYN 141
 Db 132 MFTSIFTLTMSVDRIYAVCHPVKALDFRTPAKKLINICIWLASGVGPIMYMAVTPQ 191
 QY 142 MFTSIFTLTMSVDRIYAVCHPVKALDFRTPAKKLINICIWLASGVGISAIVLGTKV 201
 Db 192 RDGA-VV-CTLOFPSP--SWYWDVTKICVLPFAVFPILITVCYGLMLRLRSVRLS 247
 QY 202 REDVDVTECSLQFPDDEYSW-WDLFMKICVFAVFPVLIIVCYITLMILRLKSVRLS 260
 Db 248 GSKEDKSLRITRMVLVVGAFVVCWAPIHIFVITVLDINRDPVVAALHCLTALG 307
 QY 261 GSRKDNRLRITKLVLVVAVFICTWPIHIFILVEALGSTSHSTA-ALSSYFICALG 319
 Db 308 YANSLNPIYAFDENKRCFRQLC 333
 QY 320 YTNSSLNPIYAFDENKRCFRDPC 345
 RESULT 11
 ID US-08-411-859-2 STANDARD; PRF; 372 AA.
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 AC xxxxxx
 XX
 DT
 XX Sequence 2, Application US/08411859

XX Sequence 2, Application US/08411859
 CC Patent No. 5985600
 CC GENERAL INFORMATION:
 CC APPLICANT: EVANS, CHRISTOPHER J.
 CC APPLICANT: KEITH JR., DUANE E.
 CC APPLICANT: EDWARDS, ROBERT H.
 CC TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
 CC TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
 CC TITLE OF INVENTION: PHARMACEUTICALS
 CC NUMBER OF SEQUENCES: 15
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Morrison & Foerster
 CC STREET: 755 Page Mill Road
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94304-1018
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/411,859
 CC FILING DATE:
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/929,200
 CC FILING DATE: 13-AUG-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: LITHGOW, TIMOTHY J.
 CC REGISTRATION NUMBER: 36,856
 CC REFERENCE/DOCKET NUMBER: 22000-20526.00
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-813-5600
 CC TELEFAX: 415-494-0792
 CC TELEX: 706141
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 372 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 372 AA; 40365 MW; 726402 CN;
 Query Match 56.3%; Score 1598; DB 2; Length 372;
 Best Local Similarity 66.7%; Pred. No. 2,22e-128;
 Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;
 Db 47 ALAIAITALYSAYCAVGLLGNCLVNFQIVRYTKLTATNIYIFNLALADALATSTLPFQS 106
 QY 57 AIPVITAVYSVVVGLVNSLVMFVIRYTKLTATNIYIFNLALADALVTTTPFQS 116
 Db 107 AKYLMEWPEGLLCKAVLSIDYNTMETSTFTLTMSVDRIYAVCHPVKALDFRTPAK 166
 QY 117 AVYLMNSWPFQGLCKIVISIDYNTMETSTFTLTMSVDRIYAVCHPVKALDFRTPAK 176
 Db 167 LINICIWLASGVGPIMYMAVTPQDGA-VV-CMLQFPSP--SWYWDVTKICVLPFAF 222
 QY 177 IINICIWLASGVGISAIVLGTKVREDVDVTECSLQFPDDEYSW-WDLFMKICVFPFAF 235
 Db 223 VVPLIITVCYGLMLRLRSVRLSGSKEDKSLRITRMVLVVGAFVVCWAPIHIFVI 282
 QY 236 VIPVLIIVCYITLMILRLKSVRLSGSKEDKSLRITRMVLVVGAFVVCWAPIHIFIL 295
 Db 283 VVITVLDINRDPVVAALHCLTALGANSINLPVYAFDENKRCFRQLCPTCPGQEP 342
 QY 296 VVALGSTSHSTA-ALSSYFICALGTNSINLPVYAFDENKRCFRDPCFTKMER 354
 Db 343 GSLRRPQA 351
 QY 355 QSTNRVNT 363

RESULT 12
ID US-08-411-859-10 STANDARD; PRT; 372 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
XX
Sequence 10, Application US/08411859
Sequence 10, Application US/08411859
Patent No. 5985600
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH JR., DUANE E.
APPLICANT: EDWARDS, ROBERT H.
TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
TITLE OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411.859
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/929,200
FILING DATE: 13-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: LITWOW, TIMOTHY J.
REGISTRATION NUMBER: 36,856
REFERENCE/DOCKET NUMBER: 22000-20526.00
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE 372 AA; 40561 MW; 727422 CN;
Query Match 56.3%; Score 1597; DB 2; Length 372;
Best Local Similarity 66.7%; Pred. No. 2,72e-128;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;
Db 47 ALAIAITALYSACVGLLGNVLNVEGIVRYTKLKTATNIYIFNLALADALATSTLPFOS 106
QY 57 AIPVITAVISVYVGVGLVGNLSLVFVIIRYTKMTATNIYIFNLALADALVTTMPFOS 116
Db 107 AKYLETWPGELLCVAVLSIDYNNFTSIFLTMMSDVRYTAVCHPVKALDFRTPAKAK 166
QY 117 AYLMMNSWFGDVLCKIVSIDYNNFTSIFLTMMSDVRYTAVCHPVKALDFRTPAKAK 176
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QY 177 IINCITWLLASSGISAIVLGCTKVEDVDVIECSLQFPDDEYSW-WDLFMKICVFPVFAF 235
Db 223 VVPIIITVCYGLMLRLSLGSGKEKDRSLRITRMVLVWYGAFVVCWAPIHIFVI 282

QY 236 VIPVLIIVCYTLMILRLKSVRLSGSREKDRNRRTKLVVVVAVFICWTIHFIL 295
Db 283 VWTIVDINRRDPLVVAALHLCIALGYANSSLNPLYIAFLDENFKCFRQLCRFCGRQEP 342
QY 296 VEALGSTSHSTA-ALSSVYFOIALGYINSSLNPLYIAFLDENFKCFRDFCFPIKMRMR 354
Db 343 GSLRRPQA 351
QY 355 QSTNRVRNT 363
RESULT 13
ID US-08-911-245-6 STANDARD; PRT; 372 AA.
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AC xxxxxx
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DT
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XX
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Sequence 6, Application US/08911245
Sequence 6, Application US/08911245
Patent No. 5821067
GENERAL INFORMATION:
APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911.245
FILING DATE: 15-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149093
FILING DATE: 06-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5821067nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
MOLECULE TYPE: protein
NAME/KEY: Protein
LOCATION: 1..372
OTHER INFORMATION: /label= Identifier
OTHER INFORMATION: /note= "Mouse Delta-Opioid Receptor"
SEQUENCE 372 AA; 40617 MW; 728086 CN;
Query Match 56.1%; Score 1593; DB 2; Length 372;
Best Local Similarity 66.7%; Pred. No. 6.18e-128;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

Db 47 ALAIAITATYSAVCAYGLIGNVLMGLIVRYTKLKTATNIYFNALADALATSTLPFOS 106
QY 57 AIPVITATYSAVGVVGLVGNLSVMEVIRYTKMKTATNIYFNALADALATSTLPFOS 116
Db 107 AXYLMTWTFEGELLCKAVLSIDYNNFTSIFTLTMMSDVDRIYAVCHPVKALDFTPAKAK 166
QY 117 AYVLNMSWFGDLCKIVISIDYNNFTSIFTLTMMSDVDRIYAVCHPVKALDFTPAKAK 176
Db 167 LINICHLWLASGVGPIVMYVMTQPR--DFAVV-CMLQFPSP--SWWDIVTKICVFPAF 222
QY 177 LINICHLWLASGVSAIVLGTKVREDVDIECSLQFPDDEYSW-WDLFMKICVFVPAF 235
Db 223 VVPIILITVYCYGLMLRLRSVRLSSGSKDRSLRITRMVLVWVGAFFVVCWAPIHIFVI 282
QY 236 VIPVLIIIVCYITLMLRLKSVRLSSGSKDRSLRITRMVLVWVGAFFVVCWAPIHIFVI 295
Db 283 VMTLVDINRDRPLVVAALHCLTALGYANSNLPVLYAFDENFKRCFQRCPCGRQEP 342
QY 296 VVALGSTSHSTA-ALSSYFECIALGYNSLNPVLYAFDENFKRCFQRCPCGRQEP 354
Db 343 GSLRRPQOA 351
QY 355 QSTNVRNT 363

RESULT 14
ID US-08-149-093A-6 STANDARD; PRT; 372 AA.

XX xxxxxx

Sequence 6, Application US/08149093A

Sequence 6, Application US/08149093A

Patent No. 5658783

GENERAL INFORMATION:

APPLICANT: Bunzow, James R

APPLICANT: Grandy, David K

TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific

TITLE OF INVENTION: Opioid Receptor Gene and Uses

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,093A

FILING DATE: 06-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAM: No. 5658783nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,311

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

CC NAME/KEY: Protein
CC LOCATION: 1..372
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Mouse Delta-Opioid Receptor"
SQ SEQUENCE 372 AA; 40617 MW; 728086 CN;

Query Match 56.1%; Score 1593; DB 1; Length 372;
Best Local Similarity 56.7%; Pred. No. 6.18e-128;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Caps 5;

Db 47 ALAIAITATYSAVCAYGLIGNVLMGLIVRYTKLKTATNIYFNALADALATSTLPFOS 106
QY 57 AIPVITATYSAVGVVGLVGNLSVMEVIRYTKMKTATNIYFNALADALATSTLPFOS 116
Db 107 AXYLMTWTFEGELLCKAVLSIDYNNFTSIFTLTMMSDVDRIYAVCHPVKALDFTPAKAK 166
QY 117 AYVLNMSWFGDLCKIVISIDYNNFTSIFTLTMMSDVDRIYAVCHPVKALDFTPAKAK 176
Db 167 LINICHLWLASGVGPIVMYVMTQPR--DFAVV-CMLQFPSP--SWWDIVTKICVFPAF 222
QY 177 LINICHLWLASGVSAIVLGTKVREDVDIECSLQFPDDEYSW-WDLFMKICVFVPAF 235
Db 223 VVPIILITVYCYGLMLRLRSVRLSSGSKDRSLRITRMVLVWVGAFFVVCWAPIHIFVI 282
QY 236 VIPVLIIIVCYITLMLRLKSVRLSSGSKDRSLRITRMVLVWVGAFFVVCWAPIHIFVI 295
Db 283 VMTLVDINRDRPLVVAALHCLTALGYANSNLPVLYAFDENFKRCFQRCPCGRQEP 342
QY 296 VVALGSTSHSTA-ALSSYFECIALGYNSLNPVLYAFDENFKRCFQRCPCGRQEP 354
Db 343 GSLRRPQOA 351
QY 355 QSTNVRNT 363

RESULT 15
ID US-08-514-451A-8 STANDARD; PRT; 398 AA.

XX xxxxxx

Sequence 8, Application US/08514451A

Sequence 8, Application US/08514451A

Patent No. 5837809

GENERAL INFORMATION:

APPLICANT: Bunzow, James R.

APPLICANT: Grandy, David K.

APPLICANT: Cirelli, Olivier

APPLICANT: Reinscheid, Rainer K.

APPLICANT: No. 5837809hacker, Hans-Peter

APPLICANT: Monsma, Frederick J.

TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID

TITLE OF INVENTION: RECEPTOR LIGAND AND USES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell

ADDRESSEE: Leigh & Whinston LLP

STREET: 121 S.W. Salmon, Suite 1600

CITY: Portland

STATE: Oregon

COUNTRY: USA

ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

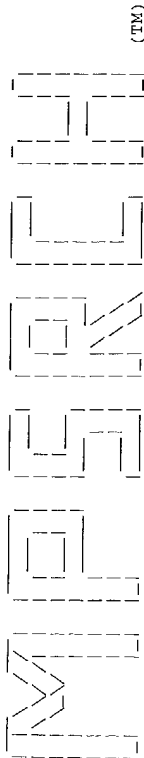
SOFTWARE: WPS.1 ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/514,451A

FILING DATE: 08/11/95

CLASSIFICATION: 435



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Feb 17 11:12:22 2000; Maspar time 19.35 Seconds

Tabular output not generated. 786.860 Million cell updates/sec

Title: >US-08-455-683-2
Description: (1-380) from US08455683.pep
Perfect Score: 2839
Sequence: 1 MESPIQIFRGDPGPTCPSA.....RNTVQDPASMRDVGGMKPV 380

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1.pir1 2.pir2 3.pir3 4.pir4

Statistics: Mean 49.052; Variance 117.295; scale 0.418

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2839	100.0	380	2	A48227 kappa opioid receptor	0.00e+00
2	2829	99.6	380	2	S36143 kappa opioid receptor	0.00e+00
3	2816	99.2	380	2	JC2434 kappa-opioid receptor	0.00e+00
4	2747	96.8	380	2	JC2338 kappa opioid receptor	0.00e+00
5	2746	96.7	380	2	I37005 kappa opioid receptor	0.00e+00
6	2610	91.9	380	2	A55259 kappa opioid receptor	0.00e+00
7	1687	59.4	373	2	JF0087 delta opioid receptor	3.50e-264
8	1680	59.2	392	2	S55693 opioid receptor mu va	6.02e-263
9	1678	59.1	398	2	A57510 mu opioid receptor -	1.36e-262
10	1677	59.1	400	2	I56533 opiate receptor mu -	2.04e-262
11	1674	59.0	398	2	I56517 mu-opioid receptor -	6.91e-262
12	1659	58.4	398	2	I56504 mu opioid receptor -	3.07e-259
13	1612	56.8	372	2	I38657 delta opiate receptor	6.03e-251
14	1610	56.7	372	2	S45592 delta opioid receptor	1.36e-250
15	1608	56.6	372	2	I38532 delta opioid receptor	3.06e-250
16	1597	56.3	372	2	B48227 G protein-coupled rec	2.66e-248
17	1473	51.9	367	2	I56520 G protein-coupled rec	1.83e-246
18	1471	51.8	367	2	JC2431 opiod receptor homol	4.11e-226
19	1470	51.8	367	2	I49022 X3 opiate receptor -	6.11e-226
20	1465	51.6	370	2	S43087 orphan opioid recepto	4.67e-225
21	980	34.5	391	2	C41795 somatostatin receptor	2.26e-140
22	978	34.4	391	2	A39287 somatostatin receptor	5.01e-140
23	976	34.4	391	2	A41795 somatostatin receptor	1.11e-139

24	968	34.1	388	2	JN0605 somatostatin receptor	2.69e-138
25	963	33.9	384	2	A47249 brain-specific somato	1.97e-137
26	954	33.6	384	2	JC4629 somatostatin receptor	7.06e-136
27	936	33.0	369	2	JC2083 somatostatin receptor	9.06e-133
28	927	32.7	369	2	A45291 somatostatin receptor	3.24e-131
29	922	32.5	369	2	D41795 somatostatin receptor	2.36e-130
30	912	32.1	369	2	B41795 somatostatin receptor	1.25e-128
31	909	32.0	346	2	S29248 somatostatin receptor	4.11e-128
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35	815	28.7	418	2	A45226 somatostatin receptor	5.80e-112
36	792	27.9	328	2	I38973 G protein-coupled rec	5.00e-108
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38	734	25.9	428	2	S30508 probable G protein-co	3.89e-98
39	732	25.8	428	2	A44021 somatostatin receptor	8.52e-98
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41	629	22.2	359	2	JC1104 angiotensin II recept	2.27e-80
42	623	21.9	355	2	A45177 chemokine (C-C) recep	2.32e-79
43	617	21.7	359	2	A48857 ARI angiotensin II re	2.36e-78
44	616	21.7	359	2	S15403 angiotensin II recept	3.48e-78
45	615	21.7	359	2	A42656 angiotensin II recept	5.12e-78

ALIGNMENTS

RESULT 1
ENTRY A48227 #type complete
TITLE kappa opioid receptor 1 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 26-May-1994 #sequence_revision 26-May-1994 #text_change 10-Sep-1997
ACCESSIONS A48227; JC4138
REFERENCE A48227
#authors Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.; Reisine, T.; Bell, G.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740
#title Cloning and functional comparison of kappa and delta opioid receptors from mouse brain.
#cross-references MUID:93342064
#accession A48227
#status preliminary
#molecule_type mRNA
#residues 1-380 #label YAS
#cross-references GB:LI1063; NID:g348248; PID:g348249
REFERENCE JC4138
#authors Liu, H.C.; Lu, S.; Augustin, L.B.; Felsheim, R.F.; Chen, H.C.; Loh, H.H.; Wei, L.N.
#journal Biochem. Biophys. Res. Commun. (1995) 209:639-647
#title Cloning and promoter mapping of mouse kappa opioid receptor gene.
#cross-references MUID:95251663
#accession JC4138
#molecule_type mRNA
#residues 1-380 #label LIJ
#note The authors translated the codon CAG for residue 365 as Glu

COMMENT This receptor exists in different areas of the central and peripheral nervous systems, and mediates many physiological and pharmacological effects of opiates and opioid compounds.

GENETICS

#gene kor

brain; G protein-coupled receptor; glycoprotein; opioid peptide; phosphoprotein; transmembrane protein

#length 380 #molecular-weight 42652 #checksum 9937

Query Match 100.08; Score 2839; DB 2; Length 380;

Best Local Similarity 100.08; Pred. No. 0.00e+00;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MESPIQIFRGDPGPTCPSACLLPNSSSSFPNWAEDSNGSVGSEDCQLLSAHSIPAIPV 60

1 MESPIQIFRGDPGPTCPSACLLPNSSSSFPNWAEDSNGSVGSEDCQLLSAHSIPAIPV 60

```

Db 61 IITAVYSVFWVGLVNSLVNFVIRTKMTATNIYIFNLALADALVTTTTPFQSAVYL 120
QY 61 IITAVYSVFWVGLVNSLVNFVIRTKMTATNIYIFNLALADALVTTTTPFQSAVYL 120
Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFLTMMVSDRYAVCHPVKALDFRPLKAKIINI 180
QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFLTMMVSDRYAVCHPVKALDFRPLKAKIINI 180
Db 181 CIWLLASVGSIAVLGKTVREDVDVIECSLQPPDDDEYSWMDLFMKTCVFEAFVPIVL 240
QY 181 CIWLLASVGSIAVLGKTVREDVDVIECSLQPPDDDEYSWMDLFMKTCVFEAFVPIVL 240
Db 241 IIVCYTLMILRLKSVRLSSGSKDRNLRTITKLIVVAVFIICWTPIHIFILVEALG 300
QY 241 IIVCYTLMILRLKSVRLSSGSKDRNLRTITKLIVVAVFIICWTPIHIFILVEALG 300
Db 301 STSHSTAALSSYFICIALGYTNSLNPVLYAFLDENFKRCRDFCFPIKMRERQSTNRV 360
QY 301 STSHSTAALSSYFICIALGYTNSLNPVLYAFLDENFKRCRDFCFPIKMRERQSTNRV 360
Db 361 RNTVODPASMVDVGGMKNPV 380
QY 361 RNTVODPASMVDVGGMKNPV 380

RESULT 2
ENTRY k361143 #type complete
TITLE kappa opioid receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE #formal_1993 #sequence_revision 19-Oct-1995 #text_change
29-Jan-1999
ACCESSIONS S36143; S38825; S36102; S39015; A48789
REFERENCE S36143
#authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.
#journal FEBS Lett. (1993) 330:77-80
#title cDNA cloning and pharmacological characterization of an
opiod receptor with high affinities for
kappa-subtype-selective ligands.
#cross-references MUID:93380575
#accession S36143 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-380 #label NIS
#cross-references GB:D16534; NID:g409390; PID:d1004487; PID:g415310
REFERENCE S38825
#authors Chen, Y.; Mestek, A.; Liu, J.; Yu, L.
#journal Biochem. J. (1993) 295:625-628
#title Molecular cloning of a rat kappa opioid receptor reveals
sequence similarities to the mu and delta opioid receptors.
#accession S38825 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-380 #label CHE
#cross-references GB:L22001; NID:g409236; PID:g409237
REFERENCE S36102
#authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.;
Onogi, T.; Kaneko, S.; Satoh, M.
#journal FEBS Lett. (1993) 329:291-295
#title Cloning and expression of a cDNA for the rat kappa-opioid
receptor.
#cross-references MUID:93374033
#accession S36102
#molecule_type mRNA
#residues 1-41, 'L', 43-380 #label MIN
#cross-references GB:D16829; NID:g404115; PID:d1004628; PID:g404116
REFERENCE S39015
#authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Dieriel, J.K.; Ashby,
B.; Liu-Chen, L.Y.
#journal Biochem. J. (1993) 295:629-633
#title Molecular cloning and expression of a rat kappa opioid
receptor.
#accession S39015

```

```

#molecule_type mRNA
#residues 1-344, 'Y', 346-380 #label LIS
REFERENCE A48789
#authors Meng, F.; Xie, G.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958
#title Cloning and pharmacological characterization of a rat kappa
opiod receptor.
#cross-references MUID:94052210
#accession A48789
#status preliminary; translated from GE/EMBL/DBJ
#molecule_type mRNA
#residues 1-380 #label RES
#cross-references EMBL:U00442; NID:g403486; PID:g403487
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 380 #molecular-weight 42688 #checksum 9972

Query Match 99.6%; Score 2829; DB 2; Length 380;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 375; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 MESPIQIFRGPGTCAPSACLLPNSSSWFFNWAESDSNGSVGSDQOLEPAHISPAIPV 60
QY 1 MESPIQIFRGPGTCAPSACLLPNSSSWFFNWAESDSNGSVGSDQOLEPAHISPAIPV 60
Db 61 IITAVYSVFWVGLVNSLVNFVIRTKMTATNIYIFNLALADALVTTTTPFQSAVYL 120
QY 61 IITAVYSVFWVGLVNSLVNFVIRTKMTATNIYIFNLALADALVTTTTPFQSAVYL 120
Db 121 MNSWPFQDVLCKIVISIDYNNMFTSIFLTMMVSDRYAVCHPVKALDFRPLKAKIINI 180
QY 121 MNSWPFQDVLCKIVISIDYNNMFTSIFLTMMVSDRYAVCHPVKALDFRPLKAKIINI 180
Db 181 CIWLLASVGSIAVLGKTVREDVDVIECSLQPPDDDEYSWMDLFMKTCVFEAFVPIVL 240
QY 181 CIWLLASVGSIAVLGKTVREDVDVIECSLQPPDDDEYSWMDLFMKTCVFEAFVPIVL 240
Db 241 IIVCYTLMILRLKSVRLSSGSKDRNLRTITKLIVVAVFIICWTPIHIFILVEALG 300
QY 241 IIVCYTLMILRLKSVRLSSGSKDRNLRTITKLIVVAVFIICWTPIHIFILVEALG 300
Db 301 STSHSTAALSSYFICIALGYTNSLNPVLYAFLDENFKRCRDFCFPIKMRERQSTNRV 360
QY 301 STSHSTAALSSYFICIALGYTNSLNPVLYAFLDENFKRCRDFCFPIKMRERQSTNRV 360
Db 361 RNTVODPASMVDVGGMKNPV 380
QY 361 RNTVODPASMVDVGGMKNPV 380

RESULT 3
ENTRY JC2434 #type complete
TITLE kappa-opioid receptor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE #formal_1995 #sequence_revision 05-Apr-1995 #text_change
05-Apr-1995
ACCESSIONS JC2434
REFERENCE JC2434
#authors Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi,
T.
#journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357
#title Structure and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opiod receptor homologue
(MOR-C).
#cross-references MUID:95100967
#accession JC2434
#molecule_type mRNA
#residues 1-380 #label NIS
#cross-references DDBJ:D31663
GENETICS
#map_position 1A2-3
#introns 86/2; 204/1
KEYWORDS kappa-opioid receptor
SUMMARY #length 380 #molecular-weight 42630 #checksum 9705

```


Query Match 99.2%; Score 2816; DB 2; Length 380;
 Best Local Similarity 99.5%; Pred. No. 0.00e+00;
 Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Db 1 MESPIQIFRGDPGPTCPSACLLPNSSSWF2NWAESDNGSVGSDQOLESAAHISPAIPV 60
QY 1 MESPIQIFRGDPGPTCPSACLLPNSSSWF2NWAESDNGSVGSDQOLESAAHISPAIPV 60

Db 61 IITAVYSVVFVGLVGNLSVMEVIIRYTKMTATNIYIFNLALADALVTMTMPFQSAYVL 120
QY 61 IITAVYSVVFVGLVGNLSVMEVIIRYTKMTATNIYIFNLALADALVTMTMPFQSAYVL 120

Db 121 MNSWPFQGVLCVKIVISIDYNNFTSIFLTMTMSVDRIYAVCHPVKALDFRPLKAKIINI 180
QY 121 MNSWPFQGVLCVKIVISIDYNNFTSIFLTMTMSVDRIYAVCHPVKALDFRPLKAKIINI 180

Db 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWMDLFMKICVFAFVIPVL 240
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWMDLFMKICVFAFVIPVL 240

Db 241 IIVCYITLMILRLKSVRLSGSREKDRNLRIITKLVLVWVAVFICWTPPIHIFILVEALG 300
QY 241 IIVCYITLMILRLKSVRLSGSREKDRNLRIITKLVLVWVAVFICWTPPIHIFILVEALG 300

Db 301 STSHSTAALSSYYFCIALGYTNSLNPNVLYAFLDENFKRCFRDPCFPKMKMERQSTNRV 360
QY 301 STSHSTAALSSYYFCIALGYTNSLNPNVLYAFLDENFKRCFRDPCFPKMKMERQSTNRV 360

Db 361 RNTVQDPASMRDVGGMKNPV 380
QY 361 RNTVQDPASMRDVGGMKNPV 380

```

```

RESULT 4
ENTRY JC2338 #type complete
TITLE kappa opioid receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
10-Sep-1997

ACCESSIONS JC2338; A55354
REFERENCE JC2338
#authors Manasson, E.; Bare, L.; Yang, D.
#journal Biochem. Biophys. Res. Commun. (1994) 202:1431-1437
#title Isolation of a human kappa opioid receptor cDNA from placenta
#cross-references MUTID:94338360
#accession JC2338
#molecule_type mRNA
#residues 1-380 #label MAN
#experimental_source placenta
REFERENCE A55354
#authors Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.
#journal J. Biol. Chem. (1994) 269:25966-25969
#title Human kappa opiate receptor second extracellular loop elevates dynorphin's affinity for human mu/kappa chimeras.
#cross-references MUTID:95014415
#accession A55354
#status preliminary
#molecule_type mRNA
#residues 136-279 #label WAN
#cross-references GB:I36130; NID:g598184; PID:g598185
COMMENT This receptor preferentially binds to dynorphins.
KEYWORDS G protein-coupled receptor; receptor; transmembrane protein
FEATURE
60-65 #domain transmembrane #status predicted #label TM1\
95-114 #domain transmembrane #status predicted #label TM2\
133-154 #domain transmembrane #status predicted #label TM3\
177-199 #domain transmembrane #status predicted #label TM4\
226-251 #domain transmembrane #status predicted #label TM5\
275-296 #domain transmembrane #status predicted #label TM6\
311-333 #domain transmembrane #status predicted #label TM7\
SUMMARY #length 380 #molecular-weight 42659 #checksum 8304

```

Query Match 96.8%; Score 2747; DB 2; Length 380;
 Best Local Similarity 93.9%; Pred. No. 0.00e+00;
 Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

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Db 1 MESPIQIFRGDPGPTCAPSACLLPNSSSAWFPQWAEPSDNGSAGSDAQLEPAHISPAIPV 60
QY 1 MESPIQIFRGDPGPTCAPSACLLPNSSSAWFPQWAEPSDNGSAGSDAQLEPAHISPAIPV 60

Db 61 IITAVYSVVFVGLVGNLSVMEVIIRYTKMTATNIYIFNLALADALVTMTMPFQSAYVL 120
QY 61 IITAVYSVVFVGLVGNLSVMEVIIRYTKMTATNIYIFNLALADALVTMTMPFQSAYVL 120

Db 121 MNSWPFQGVLCVKIVISIDYNNFTSIFLTMTMSVDRIYAVCHPVKALDFRPLKAKIINI 180
QY 121 MNSWPFQGVLCVKIVISIDYNNFTSIFLTMTMSVDRIYAVCHPVKALDFRPLKAKIINI 180

Db 181 CIWLLSSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWMDLFMKICVFAFVIPVL 240
QY 181 CIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWMDLFMKICVFAFVIPVL 240

Db 241 IIVCYITLMILRLKSVRLSGSREKDRNLRIITKLVLVWVAVFICWTPPIHIFILVEALG 300
QY 241 IIVCYITLMILRLKSVRLSGSREKDRNLRIITKLVLVWVAVFICWTPPIHIFILVEALG 300

Db 301 STSHSTAALSSYYFCIALGYTNSLNPNVLYAFLDENFKRCFRDPCFPKMKMERQSTNRV 360
QY 301 STSHSTAALSSYYFCIALGYTNSLNPNVLYAFLDENFKRCFRDPCFPKMKMERQSTNRV 360

Db 361 RNTVQDPAYLRDIDGMKNPV 380
QY 361 RNTVQDPASMRDVGGMKNPV 380

```

```

RESULT 5
ENTRY I57005 #type complete
TITLE opioid receptor kappa-1 - human
ORGANISM #formal_name Homo Sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
29-Aug-1997

ACCESSIONS I57005
REFERENCE I57005
#authors Zhu, J.; Chen, C.; Xue, J.
#journal Life Sci. (1995) 56:201-207
#title Cloning of a human kappa-opioid receptor from the brain.
#accession I57005
#status preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues 1-380 #label RES
#cross-references GB:I37362; NID:g722617; PID:g722618

GENETICS
#gene GDB:OPRK1; KOR
#cross-references GDB:I32651; OMIM:165196
#map_position 8q11.2-8q11.2
SUMMARY #length 380 #molecular-weight 42645 #checksum 8302

```

Query Match 96.7%; Score 2746; DB 2; Length 380;
 Best Local Similarity 93.7%; Pred. No. 0.00e+00;
 Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

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Db 1 MDSPIQIFRGDPGPTCAPSACLLPNSSSAWFPQWAEPSDNGSAGSDAQLEPAHISPAIPV 60
QY 1 MDSPIQIFRGDPGPTCAPSACLLPNSSSAWFPQWAEPSDNGSAGSDAQLEPAHISPAIPV 60

Db 61 IITAVYSVVFVGLVGNLSVMEVIIRYTKMTATNIYIFNLALADALVTMTMPFQSAYVL 120
QY 61 IITAVYSVVFVGLVGNLSVMEVIIRYTKMTATNIYIFNLALADALVTMTMPFQSAYVL 120

Db 121 MNSWPFQGVLCVKIVISIDYNNFTSIFLTMTMSVDRIYAVCHPVKALDFRPLKAKIINI 180
QY 121 MNSWPFQGVLCVKIVISIDYNNFTSIFLTMTMSVDRIYAVCHPVKALDFRPLKAKIINI 180

Db 181 CIWLLSSVGISAIVLGGTKVREDVDVIECSLQFPDDDEYSWMDLFMKICVFAFVIPVL 240

```


[illegible]

```

##residues      1-50,'N',52-233,'V',235-400 ##label WAN
##cross-references GB:L25119; NID:g452072; PID:g452073
REFERENCE
S41075
#authors      Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;
              Griffin, C.A.; Uhl, G.R.
#journal      FEBS Lett. (1994) 338:217-222
#title        Human mu opiate receptor. cDNA and genomic clones,
              pharmacologic characterization and chromosomal assignment.
#cross-references MUID:94139928
#accession    S41075
##status      nucleic acid sequence not shown
##molecule_type mRNA
##residues    1-50,'N',52-400 ##label WA2
REFERENCE
S51215
#authors      Bare, L.A.; Mansson, E.; Yang, D.
#journal      FEBS Lett. (1994) 354:213-216
#title        Expression of two variants of the human mu opioid receptor
              mRNA in SK-N-SH cells and human brain.
#cross-references MUID:95046336
#accession    S51215
##status      preliminary
##molecule_type mRNA
##residues    387-400 ##label BAR
GENETICS
#gene         GDB:OPRM1
##cross-references GDB:137216; OMIM:600018
#map_position 6q24-6q25
KEYWORDS      G protein-coupled receptor; glycoprotein; transmembrane
              protein
FEATURE
73-96         #domain transmembrane #status predicted #label TMX1\
107-132       #domain transmembrane #status predicted #label TMX2\
144-165       #domain transmembrane #status predicted #label TMX3\
188-208       #domain transmembrane #status predicted #label TMX4\
236-257       #domain transmembrane #status predicted #label TMX5\
283-304       #domain transmembrane #status predicted #label TMX6\
323-342       #domain transmembrane #status predicted #label TMX7\
9,12,33,40,48 #binding-site carbohydrate (Asn) (covalent) #status
              predicted
SUMMARY       #length 400 #molecular-weight 44779 #checksum 3741
Query Match   59.1%; Score 1677; DB 2; Length 400;
Best Local similarity 66.6%; Pred No. 2,04e-262;
Matches 207; Conservative 55; Mismatches 49; Indels 3; Gaps 3;
Db 70 ATTIMALYSICVVGFLGNFLVMYIVYRKMKTATNIYIFNLADALASTLPFQSVN 129
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 59 PVIIITAVSVVGVVGLVGNLWVFIIRYTKMTATNIYIFNLADALVITTMFQSAV 118
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 130 YLMGTWPGTILCKIVISIDYNNMTSFTLTCTMSVDRIYVCHPVKALDPTPNAKII 189
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 119 YLMNSWPGDVLCKIVISIDYNNMTSFTLTCTMSVDRIYVCHPVKALDPTPLKAKII 178
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 190 NVCNKLSSAIGLPVMEATKYRQG-S-IDCTLFESPTW-YWENLLKICVFIEAFITMP 246
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 179 NICHILLASSVIGSIVGKIVRDVDVIECSIQPDDEISWDLFWKICVFEAFVIP 238
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 247 VLIITVCYGLMLRLKSVMLSGSKEDKRNLRITRMVLVVVAVFVTCWTPHIYVILKA 306
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 239 VLIITVCYGLMLRLKSVMLSGSKEDKRNLRITRMVLVVVAVFVTCWTPHIYVILVEA 298
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 307 LVPTIEITFQVSWHFCIALGYNSCLNPVLYAFIDENFKCFRCFPTSSNIEQNST 366
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 299 LGSTSHSTAALSSYFFICALGYNSLSNPVLYAFIDENFKCFRCFPTPKRMERQSTN 358
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 367 RIRQNRDHPHS 377
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 359 RVRNTVQDPAS 369
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
RESULT 11
ENTRY   I56517 #type complete
TITLE   mu-opioid receptor - rat

```

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ORGANISM      #formal_name Rattus norvegicus #common_name Norway rat
DATE          26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS    I56517; I57951; A49680; I52314; S34593; A48799; I58154
REFERENCE     I56517
#authors      Bunzow, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Ronnekleiv,
              O.K.; Kelly, M.J.; Grandy, D.K.
#journal      J. Neurochem. (1995) 64:14-24
#title        Characterization and distribution of a cloned rat mu-opioid
              receptor.
#cross-references MUID:95096825
#accession    I56517
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues    1-398 ##label RES
##cross-references EMBL:U02083; NID:g403573; PID:g403574
REFERENCE     I57951
#authors      Chen, Y.; Mestek, A.; Liu, J.; Hurley, J.A.; Yu, L.
#journal      Mol. Pharmacol. (1993) 44:8-12
#title        Molecular cloning and functional expression of a mu-opioid
              receptor from rat brain.
#cross-references MUID:93341493
#accession    I57951
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues    1-398 ##label RE2
##cross-references GB:L13069; NID:g348250; PID:g348251
REFERENCE     A49680
#authors      Eppler, C.M.; Hulmes, J.D.; Wang, J.B.; Johnson, B.; Corbett,
              M.; Luthin, D.R.; Uhl, G.R.; Linden, J.
#journal      J. Biol. Chem. (1993) 268:26447-26451
#title        Purification and partial amino acid sequence of a mu opioid
              receptor from rat brain.
#cross-references MUID:94075333
#accession    A49680
##status      preliminary
##molecule_type protein
##residues    272-291 ##label EPP
##experimental_source brain membranes
##note         sequence extracted from NCBI backbone (NCBIP:140841)
REFERENCE     I52314
#authors      Sedgi, M.; Roy, S.; Ramakrishnan, S.; Elde, R.; Loh, H.H.
#journal      Biochem. Biophys. Res. Commun. (1995) 209:563-574
#title        Complementary DNA cloning of a mu-opioid receptor from rat
              peritoneal macrophages.
#cross-references MUID:95251654
#accession    I52314
##status      preliminary
##molecule_type mRNA
##residues    101-340 ##label SED
##cross-references GB:S77863; NID:g998526
##experimental_source Sprague Dawley, peritoneal macrophages
REFERENCE     S34592
#authors      Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
#journal      FEBS Lett. (1993) 327:311-314
#title        Primary structures and expression from cDNAs of rat opioid
              receptor delta- and mu-subtypes.
#cross-references MUID:93351652
#accession    S34593
##status      preliminary
##molecule_type mRNA
##residues    1-244,'V',246-398 ##label FUK
##cross-references GB:D16349; NID:g391866; PID:dl004368; PID:g391867
REFERENCE     A48799
#authors      Wang, J.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10230-10234
#title        Mu opiate receptor: cDNA cloning and expression.
#cross-references MUID:94052137
#accession    A48799
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues    1-244,'V',246-398 ##label WAN
##cross-references GB:L20684; NID:g409149; PID:g409150
REFERENCE     I58154

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```
#authors Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.
#journal Neuron (1993) 11:903-913
#title Cloning and pharmacological characterization of a rat mu
         opioid receptor.
#cross-references MUID:94059360
#accession I58154
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-244, 'V', 246-398 #label THO
#cross-references GB:I22455; NID:g437871; PID:g437672
GENETICS MUORI
#gene G protein-coupled receptor; transmembrane protein
KEYWORDS #length 398 #molecular-weight 44508 #checksum 8374
SUMMARY
Query Match 59.0%; Score 1674; DB 2; Length 398;
Best Local Similarity 65.8%; Pred. No. 6.91e-262;
Matches 208; Conservative 54; Mismatches 50; Indels 4; Gaps 4;
Db 68 AITTMALSYICVGVGLFGNFMVYVIRYTKMKTATNIYFNALADALATSTLPFQSVN 127
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 59 PVIIITAVSYVGVGLVGNLWVFIIRYTKMKTATNIYFNALADALATSTLPFQSAV 118
Db 128 YLMGTWPGTILCKIVISIDYNNMFTSIFTLCMTSDRYIAVCHPVKALDFTPRNAKIV 187
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 119 YLMNSWPGDVLCKIVISIDYNNMFTSIFTLCMTSDRYIAVCHPVKALDFTPRNAKII 178
Db 188 NVCNWLSSAIGLPMFMATKYRG-S-IDCTLFFSPTW-YWENLLKICVIFAFIMP 244
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 179 NICIWLASSVIGSAIVLGGKVRDVEDVIECSLOFPDDEYSWDLFMKICVVFVAFVIP 238
Db 245 VLIITVCYGLMILRLKSVRLSSGSEKDRNLRRIRRMVIVVAVIVCWTPPHIIVILKA 304
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 239 VLIITVCYGLMILRLKSVRLSSGSEKDRNLRRIRRMVIVVAVIVCWTPPHIIVILVEA 298
Db 305 LITIPETTFQVSWHFCALGYNSCLNPVLYAFDENKRCFRFCPTSTSTIEQQNST 364
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 299 LGSISHSTAALSSYFFCALGYNSCLNPVLYAFDENKRCFRFCPTSTSTIEQQNST 358
Db 365 RVRONTREHPSTANTV 380
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 359 RVR-NTVQDPASMRDV 373
RESULT 12
ENTRY I56504 #type complete
TITLE mu opioid receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I56504
REFERENCE I56504
#authors Zastawny, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos,
         J.; Briones-Urbina, R.; O'Dowd, B.F.
#journal J. Neurochem. (1994) 62:2099-2105
#title Cloning, characterization, and distribution of a mu-opioid
         receptor in rat brain.
#cross-references MUID:94246380
#accession I56504
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-398 #label RES
#cross-references EMBL:U35424; NID:g1017731; PID:g1017732
SUMMARY #length 398 #molecular-weight 44403 #checksum 8604
Query Match 58.4%; Score 1659; DB 2; Length 398;
Best Local Similarity 65.8%; Pred. No. 3.07e-259;
Matches 208; Conservative 53; Mismatches 51; Indels 4; Gaps 4;
Db 68 AITTMALSYICVGVGLFGNFMVYVIRYTKMKTATNIYFNALADALATSTLPFQSVN 127
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Qy 59 PVIIITAVSYVGVGLVGNLWVFIIRYTKMKTATNIYFNALADALATSTLPFQSAV 118
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Db 128 YLMGTWPGTILCKIVISIDYNNMFTSIFTLCMTSDRYIAVCHPVKALDFTPRNAKIV 187
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Qy 119 YLMNSWPGDVLCKIVISIDYNNMFTSIFTLCMTSDRYIAVCHPVKALDFTPRNAKII 178
Db 188 NVCNWLSSAIGLPMFMATKYRG-S-IDCTLFFSPTW-YWENLLKICVIFAFIMP 244
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 179 NICIWLASSVIGSAIVLGGKVRDVEDVIECSLOFPDDEYSWDLFMKICVVFVAFVIP 238
Db 245 VLIITVCYGLMILRLKSVRLSSGSEKDRNLRRIRRMVIVVAVIVCWTPPHIIVILKA 304
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 239 VLIITVCYGLMILRLKSVRLSSGSEKDRNLRRIRRMVIVVAVIVCWTPPHIIVILVEA 298
Db 305 LITIPETTFQVSWHFCALGYNSCLNPVLYAFDENKRCFRFCPTSTSTIEQQNST 364
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 299 LGSISHSTAALSSYFFCALGYNSCLNPVLYAFDENKRCFRFCPTSTSTIEQQNST 358
Db 365 RVRONTREHPSTANTV 380
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 359 RVR-NTVQDPASMRDV 373
RESULT 13
ENTRY I38657 #type complete
TITLE delta opiate receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I38657
REFERENCE I38657
#authors Simonin, F.; Befort, K.; Gaveriaux-Ruff, C.; Matthes, H.;
         Napeey, V.; Lannes, B.; Micheletti, G.; Kieffer, B.
#journal Mol. Pharmacol. (1994) 46:1015-1021
#title The human delta-opioid receptor: genomic organization, cDNA
         cloning, functional expression, and distribution in human
         brain.
#cross-references MUID:95107267
#accession I38657
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-372 #label RES
#cross-references EMBL:U10504; NID:g501144; PID:g501145
SUMMARY #length 372 #molecular-weight 40368 #checksum 1688
Query Match 56.8%; Score 1612; DB 2; Length 372;
Best Local Similarity 63.1%; Pred. No. 6.03e-251;
Matches 217; Conservative 60; Mismatches 56; Indels 9; Gaps 8;
Db 15 LFANASDAYPS-A-CPSAGANASGPPGARSAS-SLALAIAITATLYSAVCAYGLLGNVLWM 71
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 22 LLPNSSWEPNWAESDSNGSVGSEDDQLESAHISPAIPVITATYISVVFVGLVGNLSVM 81
Db 72 FGIVRYTKMKTATNIYFNALADALATSTLPFQSAKYLMTWPFGLLCAVLISIDYN 131
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 82 FVIIRYTKMKTATNIYFNALADALATSTLPFQSAVYVLMNSWPGDVLCKIVISIDYN 141
Db 132 METSIFILTMMSVDRIYAVCHPVKALDFTPRPAKLINICIWLASGVGVPIWMTYRTP 191
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 142 METSIFILTMMSVDRIYAVCHPVKALDFTPRPAKLINICIWLASGVGVPIWMTYRTP 201
Db 192 RDGA-VV-CMLQFPSP--SWYDWVTIKCVLFVAFVVFVPIITVTCYGLMLRLKSVRLS 247
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 202 REDVDVIECSLOFPDDEYSW-WDLFMKICVVFVAFVPIVILVICYVLMILRLKSVRLS 260
Db 248 GSKEDKRLRLRITRMVIVVGVAFVWNAPIHIFIVVWTLVDIDRDPVLWAAALHICIALG 307
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 261 GSKEDKRLRLRITRMVIVVGVAFVWNAPIHIFIVVWTLVDIDRDPVLWAAALHICIALG 319
Db 308 YANSSLPVLYAFDENKRCFRQLCRKPCGRPDPSFSRAREA 351
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 320 YTNSSLPVLYAFDENKRCFRQLCRKPCGRPDPSFSRAREA 363
RESULT 14
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ENTRY          S34592      #type complete
TITLE          delta opioid receptor - rat
ORGANISM       #formal_name Rattus norvegicus #common_name Norway rat
DATE           10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
                29-Jan-1999
ACCESSIONS     S34592; I56571
REFERENCE       Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
                PNAS Lett. (1993) 327:311-314
                Primary structures and expression from cDNAs of rat opioid
                receptor delta- and mu-subtypes.
#cross-references MIM:93351652
#accession      S34592
#molecule_type mRNA
#residues       1-372 #label FUK
#cross-references GB:D16348; NID:g391864; PID:d1004367; PID:g391865
REFERENCE       I56571
                Abood, M.E.
                J. Neurosci. Res. (1994) 27:714-719
                Molecular cloning and expression of a rat delta opioid
                receptor from rat brain.
#accession      I56571
#status         preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues       1-372 #label RES
#cross-references EMBL:U00475; NID:g403488; PID:g514211
GENETICS        dcl1
#gene           G protein-coupled receptor; transmembrane protein
KEYWORDS        #length 372 #molecular-weight 4049 #checksum 2221
SUMMARY         Query Match          56.7%; Score 1610; DB 2; Length 372;
                Best Local Similarity 65.6%; Pred. No. 1.36e-250;
                Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;

Db 15 LLANVSDTFPSAPFSANASGSPGAR--SAS-SLALATATATLYSACVAGLLGNVLYM 71
QY 22 LLPNSSWFPNWAESDNGSGVEDQQLSAHISPAIPVIITAVYVVFVGLVGNLSLYM 81
Db 72 FGIVRTKTKTATNIYIFNLALADALATSTLPFQSAKYLMEWTFGELCKAVLSIDYIN 131
QY 82 FVIIRYTKMTATNIYIFNLALADALVTTMPFQSAVILMNSWPGDVLCKIVISIDYIN 141
Db 132 MFTSITLTMTMSVDRIYAVCHPVKALDERTPAKALINICINIWLASGVGVPIMWAVTRP 191
QY 142 MFTSITLTMTMSVDRIYAVCHPVKALDERTPLKAKIINICINIWLASVGSISAVLGSTKV 201
Db 192 RDGA-VV-CTLOFPSP--SWYWDVTYKICVFLFAFVVPILITVVCYGLMLRLRSVRLLS 247
QY 202 REDVDVIECSLQFPDDEYSW-WDLFMKICVFFAFVFPVLIITVVCYGLMLRLRSVRLLS 260
Db 248 GSKKDRSLRRITRMVLYVGVAFVVCWAPIHIFVIVTLDINRRDPLVVAALHLCIALG 307
QY 261 GSREKDRNLRRITKLVVVAVVFIICWTPIHIFILVEALGSTSHSTA-ALSSYVFCIALG 319
Db 308 YANSSLPVLYAFLDENFKRCFRQLC 333
QY 320 YTNSSLNPVLYAFLDENFKRCFRDFC 345

RESULT 15
ENTRY          I38532      #type complete
TITLE          delta opioid receptor - human
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           29-May-1998 #sequence_revision 29-May-1998 #text_change
                29-May-1998
ACCESSIONS     I38532
REFERENCE       Knapp, R.J.; Malatynska, E.; Fang, L.; Xiaoping, L.; Nguyen,
                M.; Santoro, G.; Varga, E.V.; Hruby, V.J.; Roeske, W.R.;
                Yamamura, H.I.
                Life Sci. (1994) 54:PL463-PL469
                Identification of a human delta opioid receptor: Cloning and
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expression.
#cross-references MIM:94260835
#accession      I38532
#status         preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues       1-372 #label RES
#cross-references EMBL:U07882; NID:g497313; PID:g497314
SUMMARY         #length 372 #molecular-weight 40450 #checksum 2484
                Query Match          56.6%; Score 1608; DB 2; Length 372;
                Best Local Similarity 65.3%; Pred. No. 3.06e-250;
                Matches 213; Conservative 56; Mismatches 48; Indels 9; Gaps 8;

Db 15 LFNASDAYPS-A-PFSAGANASGPPGSGAS-SLALATATATLYSACVAGLLGNVLYM 71
QY 22 LLPNSSWFPNWAESDNGSGVEDQQLSAHISPAIPVIITAVYVVFVGLVGNLSLYM 81
Db 72 FGIVRTKTKTATNIYIFNLALADALATSTLPFQSAKYLMEWTFGELCKAVLSIDYIN 131
QY 82 FVIIRYTKMTATNIYIFNLALADALVTTMPFQSAVILMNSWPGDVLCKIVISIDYIN 141
Db 132 MFTSITLTMTMSVDRIYAVCHPVKALDERTPAKALINICINIWLASGVGVPIMWAVTRP 191
QY 142 MFTSITLTMTMSVDRIYAVCHPVKALDERTPLKAKIINICINIWLASVGSISAVLGSTKV 201
Db 192 RDGA-VV-CTLOFPSP--SWYWDVTYKICVFLFAFVVPILITVVCYGLMLRLRSVRLLS 247
QY 202 REDVDVIECSLQFPDDEYSW-WDLFMKICVFFAFVFPVLIITVVCYGLMLRLRSVRLLS 260
Db 248 GSKKDRSLRRITRMVLYVGVAFVVCWAPIHIFVIVTLDINRRDPLVVAALHLCIALG 307
QY 261 GSREKDRNLRRITKLVVVAVVFIICWTPIHIFILVEALGSTSHSTA-ALSSYVFCIALG 319
Db 308 YANSSLPVLYAFLDENFKRCFRQLC 333
QY 320 YTNSSLNPVLYAFLDENFKRCFRDFC 345

Search completed: Thu Feb 17 11:12:44 2000
Job time : 22 secs.
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W P S R E L F (TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Feb 17 11:13:01 2000; Maspar time 13.32 Seconds

Tabular output not generated. 806.224 Million cell updates/sec

Title: >US-08-455-683-2
Description: (1-380) from US08455683.pep
Perfect Score: 2839
Sequence: 1 MESPIQIPRGDPGPTCSFA.....RNTVQDPASMRDVGGMNKPV 380

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 50.173; Variance 102.089; scale 0.491

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2839	100.0	380	1	OPRK_MOUSE KAPPA-TYPE OPIOID RECE	0.00e-00
2	2829	99.6	380	1	OPRK_RAT KAPPA-TYPE OPIOID RECE	0.00e-00
3	2747	96.8	380	1	OPRK_HUMAN KAPPA-TYPE OPIOID RECE	0.00e-00
4	2610	91.9	380	1	OPRK_MOUSE MU-TYPE OPIOID RECEPTOR	0.00e-00
5	1678	59.1	398	1	OPRK_MOUSE MU-TYPE OPIOID RECEPTOR	0.00e-00
6	1677	59.0	400	1	OPRK_HUMAN MU-TYPE OPIOID RECEPTOR	0.00e-00
7	1676	59.0	398	1	OPRK_RAT MU-TYPE OPIOID RECEPTOR	0.00e-00
8	1672	58.9	401	1	OPRK_PIG MU-TYPE OPIOID RECEPTOR	0.00e-00
9	1650	58.1	401	1	OPRK_BOVIN MU-TYPE OPIOID RECEPTOR	0.00e-00
10	1612	56.8	372	1	OPRK_HUMAN DELTA-TYPE OPIOID RECEPTOR	1.71e-302
11	1610	56.7	372	1	OPRK_RAT DELTA-TYPE OPIOID RECEPTOR	1.27e-294
12	1597	56.3	372	1	OPRK_MOUSE DELTA-TYPE OPIOID RECEPTOR	3.30e-291
13	1473	51.9	367	1	OPRK_RAT NOCICEPTIN RECEPTOR (O	1.62e-291
14	1471	51.8	367	1	OPRK_MOUSE NOCICEPTIN RECEPTOR (O	7.03e-266
15	1465	51.6	370	1	OPRK_HUMAN NOCICEPTIN RECEPTOR (O	1.82e-264
16	1459	51.4	370	1	OPRK_PIG NOCICEPTIN RECEPTOR (O	3.15e-264
17	1447	51.0	370	1	OPRK_MOUSE NOCICEPTIN RECEPTOR (O	5.46e-263
18	1273	44.8	228	1	OPRK_PIG DELTA-TYPE OPIOID RECEPTOR	1.09e-224
19	980	34.5	391	1	OPRK_MOUSE SOMATOSTATIN RECEPTOR	7.81e-165
20	978	34.4	391	1	OPRK_RAT SOMATOSTATIN RECEPTOR	1.99e-165
21	976	34.4	391	1	OPRK_HUMAN SOMATOSTATIN RECEPTOR	5.06e-164
22	968	34.1	388	1	OPRK_MOUSE SOMATOSTATIN RECEPTOR	2.13e-162
23	963	33.9	384	1	OPRK_RAT SOMATOSTATIN RECEPTOR	2.20e-161

24	954	33.6	384	1	SSR4_MOUSE SOMATOSTATIN RECEPTOR	1.47e-159
25	938	33.0	368	1	SSR2_BOVIN SOMATOSTATIN RECEPTOR	2.56e-156
26	936	33.0	369	1	SSR2_PIG SOMATOSTATIN RECEPTOR	6.50e-156
27	927	32.7	369	1	SSR2_RAT SOMATOSTATIN RECEPTOR	4.32e-154
28	922	32.5	369	1	SSR2_MOUSE SOMATOSTATIN RECEPTOR	4.43e-153
29	912	32.1	369	1	SSR2_HUMAN SOMATOSTATIN RECEPTOR	4.67e-151
30	850	29.9	333	1	GRB8_HUMAN PROBABLE G PROTEIN-COU	1.52e-138
31	819	28.8	362	1	SSR5_MOUSE SOMATOSTATIN RECEPTOR	2.61e-132
32	819	28.8	363	1	SSR5_HUMAN SOMATOSTATIN RECEPTOR	2.61e-132
33	815	28.7	418	1	SSR3_HUMAN SOMATOSTATIN RECEPTOR	1.66e-131
34	792	27.9	328	1	GRP7_HUMAN PROBABLE G PROTEIN-COU	6.86e-127
35	788	27.8	363	1	SSR5_RAT SOMATOSTATIN RECEPTOR	4.35e-126
36	734	25.9	428	1	SSR3_RAT SOMATOSTATIN RECEPTOR	2.73e-115
37	732	25.8	428	1	SSR3_MOUSE SOMATOSTATIN RECEPTOR	6.85e-115
38	639	22.5	359	1	AG2R_CANFA TYPE-1 ANGIOTENSIN II	1.97e-96
39	635	22.4	359	1	OPRM_CAVPO MU-TYPE OPIOID RECEPTOR	1.21e-95
40	629	22.2	359	1	AG2R_HUMAN MU-TYPE-1A ANGIOTENSIN II	1.85e-94
41	626	22.1	359	1	AG2R_PIG TYPE-1 ANGIOTENSIN II	7.21e-94
42	623	21.9	355	1	CKR1_HUMAN C-C CHEMOKINE RECEPTOR	2.81e-93
43	617	21.7	359	1	AG2R_RABIT TYPE-1 ANGIOTENSIN II	4.27e-92
44	616	21.7	359	1	AG2R_BOVIN TYPE-1 ANGIOTENSIN II	6.72e-92
45	615	21.7	372	1	GALS_RAT GALANIN RECEPTOR TYPE	1.06e-91

ALIGNMENTS

RESULT	ID	OPRK_MOUSE	STANDARD	PRT	380 AA.
AC	P33534				
DT	01-FEB-1994 (REL. 28, CREATED)				
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).				
GN	OPRKL.				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN;				
RX	MEDLINE; 93342064.				
RA	YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,				
RA	BELL G.I.;				
RT	"Cloning and functional comparison of kappa and delta opioid				
RT	receptors from mouse brain."				
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 95100967.				
RA	NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;				
RT	"Structure and chromosomal mapping of genes for the mouse				
RT	kappa-opioid receptor and an opioid receptor homologue (MOR-C)."				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 95251663.				
RA	LIU H.C., LO S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,				
RA	LOH H.H., WEI L.N.;				
RT	"Cloning and promoter mapping of mouse kappa opioid receptor gene."				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 96084899.				
RA	BEKOWSKI S.M., ZHU J., LIU-CHEN L.Y., EISENSTEIN T.K.,				
RA	ADLER M.W., ROGERS T.J.;				
RT	"Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell				
RT	line."				
RL	J. NEUROIMMUNOL. 62:113-117(1995).				

CC -/- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

Db	241	IIIVCYTIMIRUKSVPELLSSGSEKORNERRIKLVVVAVFIIICWTPHPIILVEALG	300
QY	241	IIIVCYTIMIRUKSVPELLSSGSEKORNERRIKLVVVAVFIIICWTPHPIILVEALG	300
Db	301	STSHSTAALSSYFCIALGYTNSLSNPVLYAFDENFKCFDPCFPKMRMERQSTNRV	360
QY	301	STSHSTAALSSYFCIALGYTNSLSNPVLYAFDENFKCFDPCFPKMRMERQSTNRV	360
Db	361	RNTVQDDPASMREDVGMMKNPV	380
QY	361	RNTVQDDPASMREDVGMMKNPV	380

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RESULT      2
ID   OPK_RAT      STANDARD;      PRP;      380 AA.
AC   P34975;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN   OPK1 OR KOR-D.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC   RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
[1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 94059008.
RA   CHEN Y., MESTEK A., LIU J., YU L.;
RT   "Molecular cloning of a rat kappa opioid receptor reveals sequence
RT   similarities to the mu and delta opioid receptors.";
RL   BIOCHEM. J. 295:625-628(1993).
[2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93374033.
RA   MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
RA   KANEKO S., SATOH M.;
RT   "Cloning and expression of a cDNA for the rat kappa-opioid receptor."
RL   FEBS LETT. 329:291-295(1993).
[3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX   MEDLINE; 94059009.
RA   LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.,
RA   LIU-CHEN L.-Y.;
RT   "Molecular cloning and expression of a rat kappa opioid receptor.";
RL   BIOCHEM. J. 295:629-633(1993).
[4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX   MEDLINE; 94052210.
RA   MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
RA   WATSON S.J., AXIL H.;
RT   "Cloning and pharmacological characterization of a rat kappa opioid
RT   receptor.";
RL   PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).

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SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-BRAIN;
RX MEDLINE; 93380575.
RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.;
RT "CDNA cloning and pharmacological characterization of an opioid
RT receptor with high affinities for kappa-subtype-selective ligands.";
RN FEBS LETT. 330:77-80(1993).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE; 95204422.
RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;
RT "Structure and expression of a rat kappa opioid receptor gene.";
RN J. BIOL. CHEM. 270:16421-16424(1995).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR

FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; L22001; G409237; -
 EMBL; D16829; G404116; -
 EMBL; L22536; G425189; -
 EMBL; U00442; G403487; -
 EMBL; D16534; G415310; -
 EMBL; U17995; G727260; -
 EMBL; U17993; G727260; JOINED.
 EMBL; U17994; G727260; JOINED.
 PIR; S36143; S36143.
 PIR; S38825; S38825.
 DR GCRDB; GCR_0636; -
 DR GCRDB; GCR_0724; -
 DR GCRDB; GCR_0790; -
 DR GCRDB; GCR_0804; -
 DR GCRDB; GCR_1282; -
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
 DR PFAM; PF00001; 7tm_1; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
 FT TRANSXEM 59 85
 FT DOMAIN 86 95
 FT TRANSXEM 96 117
 FT DOMAIN 118 132
 FT TRANSXEM 133 154
 FT DOMAIN 155 173
 FT TRANSXEM 174 196
 FT DOMAIN 197 222
 FT TRANSXEM 223 247
 FT DOMAIN 248 275
 FT TRANSXEM 276 299
 FT DOMAIN 300 311
 FT TRANSXEM 312 333
 FT DOMAIN 334 380
 FT DISULFID 131 210
 FT LIPID 345 345
 FT CARBOHYD 25 25
 FT CARBOHYD 39 39
 FT CONFLICT 42 42
 FT CONFLICT 345 345
 SQ SEQUENCE 360 AA; 42688 MW; EF858A46 CRC32;

Query Match 99.6%; Score 2829; DB 1; Length 380;
 Best Local Similarity 98.9%; Pred. No. 0.004+00;
 Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Dd 1 MESPIQIFRGGPTCAPSACLLPNSSWFNPAESDNGSVGSDQOLEPAHISPAIPV 60
 Qy 1 MESPIQIFRGGPTGPTSPACLLPNSSWFNPAESDNGSVGSDQOLESAHISPAIPV 60
 Dd 61 IITAVYSVVFVGLVGNLSLVFVIIRYKMTATNIYIFNLADALVTTMPFQSAYVL 120
 Qy 61 IITAVYSVVFVGLVGNLSLVFVIIRYKMTATNIYIFNLADALVTTMPFQSAYVL 120
 Dd 121 MNSWFGDVLCKIVISIDYINMFTSIFTLIMSVDRYIAVCHPVKALDFRPLKAKIINI 180
 Qy 121 MNSWFGDVLCKIVISIDYINMFTSIFTLIMSVDRYIAVCHPVKALDFRPLKAKIINI 180
 Dd 181 CIWLASSVGISAIYLGTKVREDVDIECSLQFPDDDEYSWMDLFMKICVFVFAFVPLV 240

QY 181 CIWLASSVGISAIYLGTKVREDVDIECSLQFPDDDEYSWMDLFMKICVFVFAFVPLV 240
 Dd 241 IIVCYTTLMLKSVRLSSREKDRNLRTIKVLVVVAVFIICWTPIHIFILVEALG 300
 QY 241 IIVCYTTLMLKSVRLSSREKDRNLRTIKVLVVVAVFIICWTPIHIFILVEALG 300
 Dd 301 STSHSTAVLSYFYCFIALGYTNSSLPVLYAFLDENKRCFDFCFPKMRMEROSTNRV 360
 QY 301 STSHSTAVLSYFYCFIALGYTNSSLPVLYAFLDENKRCFDFCFPKMRMEROSTNRV 360
 Dd 361 RNTVQDPASMRDVGGMKPV 380
 QY 361 RNTVQDPASMRDVGGMKPV 380

RESULT 3
 ID OPRK_HUMAN STANDARD; PRT; 380 AA.
 AC P41145;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
 GN OPRK1 OR OPRK.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 94338360.
 RA MANSSON E., BARE L.A., YANG D.;
 RT "Isolation of a human kappa opioid receptor cDNA from placenta."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 95350200.
 RA SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,
 RA MATTEI M.-G., CHARON G., BLOCH B., KIEFFER B.;
 RT "Kappa-Opioid receptor in humans: cDNA and genomic cloning,
 RT chromosomal assignment, functional expression, pharmacology, and
 RT expression pattern in the central nervous system."
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 95174504.
 RA ZHU J., CHEN C., XUE J.-C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;
 RT "Cloning of a human kappa opioid receptor from the brain."
 RL LIFE SCI. 56:201-207(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
 CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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EMBL; U11053; G532060; -
 EMBL; U17298; G596070; -
 EMBL; L37362; G722618; -
 PIR; JC2338; JC2336.
 DR GCRDB; GCR_1819; -
 DR GCRDB; GCR_2026; -
 DR GCRDB; GCR_2054; -
 DR MIM; 165196; -

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DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM: PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58
FT TRANSMEM 59 85
FT DOMAIN 86 95
FT TRANSMEM 96 117
FT DOMAIN 118 132
FT TRANSMEM 133 154
FT DOMAIN 155 173
FT TRANSMEM 174 196
FT TRANSMEM 197 222
FT DOMAIN 223 247
FT TRANSMEM 248 275
FT DOMAIN 276 299
FT TRANSMEM 300 311
FT TRANSMEM 312 333
FT DOMAIN 334 380
FT TRANSMEM 380 426
FT DISULFID 131 210
FT LIPID 345 345
FT CARBOHYD 25 25
FT CARBOHYD 39 39
FT CONFLICT 2
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

Query Match          96.8%; Score 2747; DB 1; Length 380;
Best Local Similarity 93.9%; Pred. No. 0.00e+00;
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 1 MESPIQIFRGEPTCAPSACLPNNSAWFPQWAPDNGSAGSDEAQLPAHISPAIPV 60
QY 1 MESPIQIFRGEPTCAPSACLPNNSAWFPQWAPDNGSAGSDEAQLPAHISPAIPV 60
Db 61 IITAVSVVVGNGSLVMEVIRYTKMTATNIYFNALADALVTTTTPFQSTVYL 120
QY 61 IITAVSVVVGNGSLVMEVIRYTKMTATNIYFNALADALVTTTTPFQSTVYL 120
Db 121 MNSWFGDVLCKIVISIDYNNMETSIFLTMTMSVDRIYAVCHPKALDFTPLKAIINI 180
QY 121 MNSWFGDVLCKIVISIDYNNMETSIFLTMTMSVDRIYAVCHPKALDFTPLKAIINI 180
Db 181 CIWLLSSVGSIAVLGGTKVEDVDVIECSLQFPDDDDYSWDLFMKICVFVFAVIVL 240
QY 181 CIWLLSSVGSIAVLGGTKVEDVDVIECSLQFPDDDDYSWDLFMKICVFVFAVIVL 240
Db 241 IIVCYTLMILKSLVRLSGSKDRNLRRITRLVAVVAVVVCWTPPIHIFILVEALG 300
QY 241 IIVCYTLMILKSLVRLSGSKDRNLRRITRLVAVVAVVVCWTPPIHIFILVEALG 300
Db 301 STSHSTAALSSYFFICALGYTNSSLPILYAFLDENFKRCFRDFFPLKMRMERQSTSRV 360
QY 301 STSHSTAALSSYFFICALGYTNSSLPILYAFLDENFKRCFRDFFPLKMRMERQSTSRV 360
Db 361 RNTVQDPAYLRIDGMKPV 380
QY 361 RNTVQDPASMRDVGGMKEV 380

RESULT 4
ID OPK_CAVPO STANDARD; PRT; 380 AA.
AC P41144;
DT 01-FEB-1995 (REL. 31, CREATED)
DE 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPTOID RECEPTOR (KOR-1).
GN OPK1.
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE=BRAIN;

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RX MEDLINE; 94224925.
RA XIE G-X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
RA GOLDSTEIN A., WATSON S.J., AKIL H.;
RT "Primary structure and functional expression of a guinea pig kappa
RT opiod (dynorphin) receptor.";
RL PROC. NAIL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC CC FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U04092; G476107; -.
DR GCRDB; GCR_0991; -.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM: PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58
FT TRANSMEM 59 85
FT DOMAIN 86 95
FT TRANSMEM 96 117
FT DOMAIN 118 132
FT TRANSMEM 133 154
FT DOMAIN 155 173
FT TRANSMEM 174 196
FT DOMAIN 197 222
FT TRANSMEM 223 247
FT DOMAIN 248 275
FT TRANSMEM 276 299
FT DOMAIN 300 311
FT TRANSMEM 312 333
FT DOMAIN 334 380
FT DISULFID 131 210
FT LIPID 345 345
FT CARBOHYD 25 25
FT CARBOHYD 39 39
SQ SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;

Query Match          91.9%; Score 2610; DB 1; Length 380;
Best Local Similarity 92.9%; Pred. No. 0.00e+00;
Matches 338; Conservative 21; Mismatches 5; Indels 0; Gaps 0;

Db 17 ARNACILLNGSAWLPGWAEPPDNGSAGSDQLEPAHISPAIPVITAVSVVVGVLG 76
QY 17 SPSCALLPNSSSWFENWAEEDSDNGSVGSDQLESAHISPAIPVITAVSVVVGVLG 76
Db 77 NSLVMFVIRYTKMTATNIYFNALADALVTTTTPFQSTVILNNSWFPDGLCKIVIS 136
QY 77 NSLVMFVIRYTKMTATNIYFNALADALVTTTTPFQSTVILNNSWFPDGLCKIVIS 136
Db 137 IDYNNMETSIFLTMTMSVDRIYAVCHPKALDFTPLKAIINIWLSSVGSIAIL 196
QY 137 IDYNNMETSIFLTMTMSVDRIYAVCHPKALDFTPLKAIINIWLSSVGSIAIL 196
Db 197 GGTKVRREDVDIIECSLQFPDDDDYSWDLFMKICVFVFAVIVLIIIVCYTLMILKSLV 256
QY 197 GGTKVRREDVDIIECSLQFPDDDDYSWDLFMKICVFVFAVIVLIIIVCYTLMILKSLV 256
Db 257 RLLSGSREKDRNLRRITRLVAVVAVVVCWTPPIHIFILVEALGSTSHSTAALSSYFFCI 316
QY 257 RLLSGSREKDRNLRRITRLVAVVAVVVCWTPPIHIFILVEALGSTSHSTAALSSYFFCI 316
Db 317 ALGYTNSSLPILYAFLDENFKRCFRDFFPLKMRMERQSTSRVNTVQDPAYMRNVDGV 376

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FT	DOMAIN	1	64	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	65	94	1 (POTENTIAL).
FT	DOMAIN	95	103	1 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	104	121	2 (POTENTIAL).
FT	DOMAIN	122	143	3 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	144	163	3 (POTENTIAL).
FT	DOMAIN	164	193	4 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	194	209	4 (POTENTIAL).
FT	DOMAIN	210	234	5 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	235	257	5 (POTENTIAL).
FT	DOMAIN	258	280	6 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	281	303	6 (POTENTIAL).
FT	DOMAIN	304	311	7 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	312	328	7 (POTENTIAL).
FT	DOMAIN	329	398	8 CYTOPLASMIC (POTENTIAL).
FT	DISULFID	140	217	BY SIMILARITY.
FT	LIPID	351	351	PALMITATE (POTENTIAL).
FT	CARBOHYD	9	9	POTENTIAL.
FT	CARBOHYD	31	31	POTENTIAL.
FT	CARBOHYD	38	38	POTENTIAL.
FT	CARBOHYD	46	46	POTENTIAL.
FT	CONFLICT	22	22	C -> W (IN REF. 3).
SEQ	SEQUENCE	398 AA;	44421 MW; C0211489 CRC32;	

Query Match 59.1%; Score 1678; DB 1; Length 398;
Best Local Similarity 65.8%; Pred. No. 0.00e+00;
Matches 208; Conservative 55; Mismatches 49; Indels 4; Gaps

Db	68	ATIMALYSIVCVGLFEGFNVMYIVIRYTKMTATNIVIFNALADALATSTLPQSVN	127
QY	59	PVIAIVSYVFFVGLVGNLSVNFVIRYTKMTATNIVIFNALADALVITTPQSAV	118
Db	128	YLMGTWPFNGILCKIVISIDYNNMFTSIFLCTMSVDRIYAVCHPVKALDFRPNKIV	178
QY	119	YLMNSWPFPGVILCKIVISIDYNNMFTSIFLCTMSVDRIYAVCHPVKALDFRPLKAKII	178
Db	188	NVCNWLSSAIGLVPMFMATKYRQG-S-IDCLTFSHTW-YWENLLKICVFIFAFIMP	244
QY	179	NICILWLLASSVGISAIVLGGTKYREDVDVIECSLQFPDDDEYSWMDLFMKICVFVFAVIP	238
Db	245	VLIITVCYGLMIILRLKSVMLSGSKKDRNLRLRITRMVLVWVAVFVCGVTPHIHYVIA	304
QY	239	VLIITVCYGLMIILRLKSVRLSGSKKDRNLRLRITRMVLVWVAVFVCGVTPHIHYVIA	298
Db	305	LITIPPTFOTVSHFCIALGYNSCLNPVLYAFLDENKRCFRFCIPTSSIEQNSA	364
QY	299	LGSTSHSTAALSYFCIALGYNSCLNPVLYAFLDENKRCFRFCIPTSSIEQNSA	358
Db	365	RIRONTREHPSTANTV	380
QY	359	RVR-NIVQDPSMRDV	373

RESULT 6
ID OPRM_HUMAN STANDARD; PRI: 400 AA.
AC P35372; Q12930;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE MO-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1 OR MOR1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CAYARRHINI; HOMINIDAE; HOMO.
RN [1]
RE SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE: 94139928.
RA WANG J.-B., JOHNSON P.S., PERISCO A.M., HAWKINS A.L., GRIFFIN C.A.,
RA UHL G.R.;
RT "Human mu opiate receptor. cDNA and genomic clones, pharmacologic
RL characterization and chromosomal assignment.";
RL FEBS LETT 338:217-222(1994)

FC TISSUE-BRAIN;
 RX MEDLINE: 94246380.
 RA ZASTAWY R.L., GEORGE S.R., NGUYEN T., CHENG R., TSATSOS J.,
 RA BRIONES-ORBINA R., O'DOWD B.F.;
 RT "Cloning, characterization, and distribution of a mu-opioid receptor
 in rat brain.";
 RL J. NEUROCHEM. 62:2099-2105(1994).
 RN [7].
 RP SEQUENCE OF 101-340 FROM N.A.
 RC TISSUE-MACROPHAGE;
 RX MEDLINE: 95251654.
 RA SEDQI M., ROY S., RAMAKRISHNAN S., ELDE R., LOH H.H.;
 RT "Complementary DNA cloning of a mu-opioid receptor from rat
 peritoneal macrophages";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995).
 RN [8].
 RP SEQUENCE OF 356-391 FROM N.A.
 RX MEDLINE: 95172221.
 RA ZIMPRICH A., SIMON T., HOLLT V.;
 RT "Cloning and expression of an isoform of the rat mu opioid receptor
 (MOR1B) which differs in agonist induced desensitization from
 MOR1.";
 RL FEBS LETT. 359:142-146(1995).
 CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 FOR BETA-ENDORPHIN.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: BRAIN. IS EXPRESSED IN THE CEREBRAL CORTEX,
 CAUDATE PUTAMEN, NUCLEUS ACCUMBENS, SEPTAL NUCLEI, THALAMUS,
 HIPPOCAMPUS, AND HABENULA. NOT DETECTED IN CEREBELLUM.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: D16349; G391867; -
 DR EMBL: L20684; G409150; -
 DR EMBL: L13069; G348251; -
 DR EMBL: U02083; G403574; -
 DR EMBL: L22455; G437872; -
 DR EMBL: U35424; G1017732; -
 DR EMBL: S77863; E199500; -
 DR EMBL: S75669; G861432; -
 DR PIR: S34593; S34593.
 DR GCRDB: GCR_0633; -
 DR GCRDB: GCR_0637; -
 DR GCRDB: GCR_0839; -
 DR GCRDB: GCR_0840; -
 DR GCRDB: GCR_1101; -
 DR GCRDB: GCR_1425; -
 DR GCRDB: GCR_2361; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 DR PFAM: PF00001; 7tm1; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 64
 FT TRANSMEM 65 94
 FT DOMAIN 95 103
 FT TRANSMEM 104 121
 FT DOMAIN 122 143
 FT TRANSMEM 144 163
 FT DOMAIN 164 193
 FT TRANSMEM 194 209
 FT DOMAIN 210 234
 FT TRANSMEM 235 257
 FT DOMAIN 258 280
 FT TRANSMEM 281 303

FT DOMAIN 304 311
 FT TRANSMEM 312 328
 FT DOMAIN 329 398
 FT DISULFID 140 217
 FT LIPID 351 351
 FT CARBOHYD 9 9
 FT CARBOHYD 31 31
 FT CARBOHYD 38 38
 FT CARBOHYD 46 46
 FT CARBOHYD 53 53
 FT CONFLICT 237 237
 FT CONFLICT 245 245
 FT CONFLICT 387 391
 SQ SEQUENCE 398 AA; 44494 MW; 2C21013D CRC32;
 Query Match 59.0%; Score 1676; DB 1; Length 398;
 Best Local Similarity 66.1%; Pred. No. 0.00e+00;
 Matches 209; Conservative 53; Mismatches 50; Indels 4; Gaps 3;
 Db 58 AITMALYSIVCVYGLFCGNFLVMYVIVETKMTATNIYIENLADALATSLPFSVN 127
 Qy 59 PVIIATVSVVYVGLVGNLSVFIHYTKMTATNIYIENLADALATVITMPSQAV 118
 Db 128 YLMGTWPGIICKIVISIDYNNMFTSFTICTMSVDYIAVCHPVKALDERTPNKXIV 187
 Qy 119 YLMNSWPGDVICKIVISIDYNNMFTSFTILMMSVDYIAVCHPVKALDERTPLKAKII 178
 Db 188 NYCNIWLSAIGLPVMEFMAIKYQG-S-IDCTITFSHTW-YWENLKLKICVFIAFIMP 244
 Qy 179 NICIWLASSVIGSAIVLGGIKVREDVDVIECSLQFPDDEYSWMDLFKICVFAFVIP 238
 Db 245 VLIITVCVGLMLRLKSVMSGSKEDRNLRTRMVLVYVAVFVTCWTHIYVIKA 304
 Qy 239 VLIITVCVGLMLRLKSVMSGSKEDRNLRTRMVLVYVAVFVTCWTHIYVIKA 298
 Db 305 LITIPETQFVSWHFICALGYNTSCLNPVLYAFIDENKFCRFFCIPTSSTIEQQNST 364
 Qy 239 LGSISHSTAALSSVYFCALGYNTSCLNPVLYAFIDENKFCRFFCIPKRMVERQSTN 358
 Db 365 RVRONTREHPSTANIV 380
 Qy 359 RVR-NTVQDPASMRDV 373
 RESULT 8 STANDARD; PRT; 401 AA.
 ID OPRM_PIG
 AC Q95247;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MC-TYPE OPIOID RECEPTOR (MOR-1).
 GN OPRM1.
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN CORTEX;
 RA PAMPUSCH M.P., OSINSKI M.A., BROWN D.R., MURTAUGH M.P.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 FOR BETA-ENDORPHIN.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----

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CC -----
DR EMBL: L38645; GI553057; -.
DR GCRDB; GCR_1287; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 67 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 68 97 1 (POTENTIAL).
FT DOMAIN 98 106 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 107 124 2 (POTENTIAL).
FT DOMAIN 125 146 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 147 166 3 (POTENTIAL).
FT DOMAIN 167 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 212 4 (POTENTIAL).
FT DOMAIN 213 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 260 5 (POTENTIAL).
FT DOMAIN 261 283 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 284 306 6 (POTENTIAL).
FT DOMAIN 307 314 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 315 331 7 (POTENTIAL).
FT DOMAIN 332 401 CYTOPLASMIC (POTENTIAL).
FT LIPID 354 354 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 41 41 POTENTIAL.
FT CARBOHYD 49 49 POTENTIAL.
SQ SEQUENCE 401 AA; 45098 MW; 6786FD94 CRC32;

Query Match 58.9%; Score 1672; DB 1; Length 401;
Best Local Similarity 66.6%; Pred. No. 0.00e-00;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

Db 71 AIIIMALYSIVCVGLFGLNFMVIVRYTKMTATNIYFNALADALATSTLPQSYN 130
QY 59 PVIIITAVISVWFVGLVGNLSVYVIRYTKMTATNIYFNALADALATSTLPQSAV 118
Db 131 YLMGWPFPGTILCKIVISIDYNNMETSIFTLCTMSVDRIYAVCHPKALDFTPRNAKII 190
QY 119 YLMNSWPFGLVCKIVISIDYNNMETSIFTLTMSVDRIYAVCHPKALDFTPLKAKII 178
Db 191 NYCNWILSSAIGLPVFMATTKYRQ-S-IDCALFESHTW-YWENLLKICVFIFAFIMP 247
QY 179 NICIWLASSVGISAIVLGSTKVREDVDVIEGSLQFPDDEYSWDLFMKICVFVFAFVP 238
Db 248 VLIITVCYGLMILRLKSVRLSGSKEDRNLRITRMVLVVAVFTVCWTPTHIVKIIKA 307
QY 239 VLIITVCYGLMILRLKSVRLSGSKEDRNLRITRMVLVVAVFTVCWTPTHIVKIIKA 298
Db 308 LTIPTTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFRFCPTSTIEQONS 367
QY 299 LGSTSHSTAALSSYYFCIALGYTNSCLNPVLYAFDENFKRCFRFCPTSTIEQONS 358
Db 368 RIRQNRDHP 378
QY 359 RYRNTVQDPAS 369

RESULT 9
ID OPRM BOVIN STANDARD; PRT; 401 AA.
AC F79350;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-STRIATUM;
RA SIMON E.J., WILLEM S., ANDRIA M., ONOPRISHVILI I., HILLER J.M.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC !- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U89677; GI881731; -.
DR GCRDB; GCR_1213; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 67 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 68 97 1 (POTENTIAL).
FT DOMAIN 98 106 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 107 124 2 (POTENTIAL).
FT DOMAIN 125 146 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 147 166 3 (POTENTIAL).
FT DOMAIN 167 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 212 4 (POTENTIAL).
FT DOMAIN 213 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 260 5 (POTENTIAL).
FT DOMAIN 261 283 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 284 306 6 (POTENTIAL).
FT DOMAIN 307 314 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 315 331 7 (POTENTIAL).
FT DOMAIN 332 401 CYTOPLASMIC (POTENTIAL).
FT LIPID 354 354 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 41 41 POTENTIAL.
FT CARBOHYD 49 49 POTENTIAL.
SQ SEQUENCE 401 AA; 45045 MW; 5673B9B8 CRC32;

Query Match 58.1%; Score 1650; DB 1; Length 401;
Best Local Similarity 65.9%; Pred. No. 1.71e-302;
Matches 205; Conservative 54; Mismatches 49; Indels 3; Gaps 3;

Db 71 AIIIMALYSIVCVGLFGLNFMVIVRYTKMTATNIYFNALADALATSTLPQSYN 130
QY 59 PVIIITAVISVWFVGLVGNLSVYVIRYTKMTATNIYFNALADALATSTLPQSAV 118
Db 131 YLMGWPFPGTILCKIVISIDYNNMETSIFTLCTMSVDRIYAVCHPKALDFTPRNAKII 190
QY 119 YLMNSWPFGLVCKIVISIDYNNMETSIFTLTMSVDRIYAVCHPKALDFTPLKAKII 178
Db 191 NICNWLSSAIGLPVFMATTKYRQ-S-IDSTLFTSHTW-YWENLLKICVFIFAFIMP 247
QY 179 NICIWLASSVGISAIVLGSTKVREDVDVIEGSLQFPDDEYSWDLFMKICVFVFAFVP 238
Db 248 ILIITVCYGLMILRLKSVRLSGSKEDRNLRITRMVLVVAVFTVCWTPTHIVKIIKA 307
QY 239 VLIITVCYGLMILRLKSVRLSGSKEDRNLRITRMVLVVAVFTVCWTPTHIVKIIKA 298
Db 308 LTIPTTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFRFCPTSTIEQONS 367
QY 299 LGSTSHSTAALSSYYFCIALGYTNSCLNPVLYAFDENFKRCFRFCPTSTIEQONS 358
Db 368 RIRQNRDHP 378
QY 359 RYRNTVQDPAS 369

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RESULT 10
ID OPND_HUMAN STANDARD; PRT; 372 AA.
AC P41143;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DI 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1).
GN OPND1 OR OPND.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN CORTEX, AND STRIATUM;
RX MEDLINE; 94260835.
RA KRAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,
RA KANTOR G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.;
RT "Identification of a human delta opioid receptor: cloning and
RT expression";
RL LIFE SCI. 54:463-469(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95107267.
RA SIMONIN F., BEFORT K., GAVERIAUX-RUFFE C., MATTHES H., NAPPEY V.,
RA LANNES B., MICHELETTI G., KIEFFER B.;
RT "The human delta-opioid receptor: genomic organization, cDNA cloning,
RT functional expression, and distribution in human brain.";
RL MOL. PHARMACOL. 46:1015-1021(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX GRAHAM D.;
RA SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U07882; G497314; -.
DR EMBL; U10504; G501145; -.
DR EMBL; AL009181; E1250368; -.
DR GCRDB; GCR_1017; -.
DR GCRDB; GCR_2055; -.
DR MIM; 165195; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm.1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT DOMAIN 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT DOMAIN 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372

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FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT DISULFID 121 198 BY SIMILARITY.
FT LIPID 333 333 PALMITATE (POTENTIAL).
FT CONFLICT 27 27 C -> F (IN REF. 1).
FT CONFLICT 40 41 AR -> PG (IN REF. 1).
FT CONFLICT 348 348 A -> P (IN REF. 1).
FT CONFLICT 370 370 A -> R (IN REF. 1).
SQ SEQUENCE 372 AA; 40368 MW; 4A57DD07 CRC32;

Query Match 56.8%; Score 1612; DB 1; Length 372;
Best Local Similarity 63.1%; Pred. No. 1.27e-294;
Matches 217; Conservative 60; Mismatches 58; Indels 9; Gaps 8;

Db 15 LFNASDAYPS-A-CPSAGANASGPPGARSAS-SLAALAIATATYSAVCAYGLGNVLVM 71
QY 22 LLPNSSFFKFPNWAESDSNGSVGSDQLESASHPAIVITAVISVVVGVGLVGNLSVM 81
Db 72 FGIVRYTKMKTATNIYFNALADALATSIPLFOSAKYLMETWPFGEELCKAVLSIDYN 131
QY 82 FVIRYTKMKTATNIYFNALADALATYTMPFQSAVYLMNSWFGVGLCKIVISIDYN 141
Db 132 MFTSIFLTMMSDVRYIAVCHPVKALDPTPAKALINICIWLASGVGVPMVMVTRP 191
QY 142 MFTSIFLTMMSDVRYIAVCHPVKALDPTPAKALINICIWLASGVGISAIVLGSTKV 201
Db 192 RDGA-VV-CMLQFPSP--SWYWDIVTKICVLFAPVFPILLITVYCYGLMLRLRSVRLS 247
QY 202 REDVDVIECSLQFPDEYSW-WDLFMKICVFEVFAFVPLVLIIVCYTLMILRLSVRLS 260
Db 248 GSKKDRSLRITRMVLVVGAFVVCNAPIHFIVVTLVVDIDRRDPLVVAALHCLIALG 307
QY 261 GSREKDRNLRIKILVWVAVFICWTPIHILFVLRALGSTSHSTA-ALSSYVFCIALG 319
Db 308 YANSLNVLVYAFDENKFRQLCRKPCGRDPDPSPFSRAREA 351
QY 320 YTNSSLNVLVYAFDENKFRQCFRCFCPIKMRERQSTNVRNT 363

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RESULT 11

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ID OPND_RAT STANDARD; PRT; 372 AA.
AC P33533;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
GN OPND1 OR KOR-A.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RT "Primary structures and expression from cDNAs of rat opioid receptor
RT delta- and mu-subtypes.";
RL FEBS LETT. 327:311-314(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE; 94322412.
RA ABOOD M.E., NOEL M.A., FARNSWORTH J.S., IAO Q.;
RT "Molecular cloning and expression of a delta-opioid receptor from rat
RT brain.";
RL J. NEUROSCI. RES. 37:714-719(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; D16348; G391865; -;
 DR EMBL; U00475; G514211; -;
 DR PIR; S34592; S34592.
 DR GCRDB; GCR_0638; -;
 DR GCRDB; GCR_0805; -;
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
 DR PFAM; PF0001; 7cml_1; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 45
 FT TRANSMEM 46 75
 FT DOMAIN 76 84
 FT TRANSMEM 85 102
 FT DOMAIN 103 124
 FT TRANSMEM 125 144
 FT DOMAIN 145 174
 FT TRANSMEM 175 190
 FT DOMAIN 191 215
 FT TRANSMEM 216 238
 FT DOMAIN 239 261
 FT TRANSMEM 262 284
 FT DOMAIN 285 293
 FT TRANSMEM 294 310
 FT DOMAIN 311 372
 FT CARBOHYD 18 18
 FT CARBOHYD 33 33
 FT DISULFID 121 198
 FT LIPID 333 333
 SQ SEQUENCE 372 AA; 40449 MW; 59F5E50 CRC32;
 Query Match 56.7%; Score 1610; DB 1; Length 372;
 Best Local Similarity 65.6%; Pred. No. 3.30e-294;
 Matches 214; Conservative 55; Mismatches 48; Indels 9; Gaps 7;
 Db 15 LLNVSDFPSAFPSANASGPGAR--SAS-SLALAIALTALYSACVGLLGNVLVM 71
 QY 22 LLPNSSWFPPKAESDSGVSEDDQLESHPAIPVITAYSVFVGLVGNLSVM 81
 Db 72 FGIVRYTKLATNIYIFNLADALATSTLPFQSAKYLMTWPGELLCRAVLSDIYN 131
 QY 82 FVIRYTKMTATNIYIFNLADALATVTPFQSAVLMNSWPPGDLCKIVISDIYN 141
 Db 132 MFTSTFTLTMMSVDRIYAVCHPVKALDRTAKAKLINICLWLASGVGVLMVAVTQP 191
 QY 142 MFTSTFTLTMMSVDRIYAVCHPVKALDRTPLKAKIINICLWLASGVGISAIVLGTKV 201
 Db 192 RDGA-VV-CTIQFSP--SWWTDVTIKICVLFAPVFPVPIITVCYGLMLRLSRVLLS 247
 QY 202 REDVDVIECSQFDDDEYSW-WDFMKICVFVFAFVIFVLIIVCYTLMILRLKSVLLS 260
 Db 248 GSKEDRSRLRITRMVLVVGAFVVCWAPIHFIVYVLTVDINRDPVLVVAALHICIALG 307
 QY 261 GSREKDRNLRLRITRLVLVWVAVFICWTPFIHFILVEALGSTSHSTA-ALSSVYFCIALG 319
 Db 308 YANSLNPLVYAFLDENFKRCFROIC 333
 QY 320 YTNSSLNPLVYAFLDENFKRCFRDFC 345
 RESULT 12
 ID OPD1 MOUSE STANDARD; PRT; 372 AA.
 AC P32300;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).

GN OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC OC RUDARTIA; SCIURGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93101664.
 RA KIEFFER B.L.; BEFORT K.; GAVERIAUX-ROFF C.; HIRTH C.G.;
 RT "The delta-opioid receptor: isolation of a cDNA by expression cloning
 RL and pharmacological characterization.";
 RN PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93110361.
 RA EVANS C.J.; KEITH D.E. JR.; MORRISON H.; MAGENDZO K.; EDWARDS R.H.;
 RT "Cloning of a delta opioid receptor by functional expression.";
 RL SCIENCE 258:1952-1955(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-BRAIN;
 RX MEDLINE; 93342064.
 RA YASUDA K.; RAYNOR K.; KONG H.; BREDER C.D.; TAKEDA J.; REISINE T.;
 RA BELL G.I.;
 RT "Cloning and functional comparison of kappa and delta opioid
 RL receptors from mouse brain.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93391492.
 RA KEITH D.E. JR.; ANTON B.; EVANS C.J.;
 RT "Characterization and mapping of a delta opioid receptor clone from
 RL NG108-15 cells.";
 RL PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
 RN [5]
 RP SEQUENCE OF 8-372 FROM N.A.
 RX MEDLINE; 94022364.
 RA BZDEGA T.; CHIN H.; KIM K.; JUNG H.H.; KOZAK C.A.; KLEE W.A.;
 RT "Regional expression and chromosomal localization of the delta opiate
 RL receptor gene.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
 RN [6]
 RP 3D-STRUCTURE MODELLING.
 RX MEDLINE; 97001837.
 RA ALKORTA I.; LOEW G.H.;
 RT "A 3D model of the delta opiod receptor and ligand-receptor
 RL complexes.";
 RL PROTEIN ENG. 9:573-583(1996).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
 CC STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL
 CC GANGLIA AND LIMBIC REGIONS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; L05322; G192943; -;
 DR EMBL; L07271; -; NOT_ANNOTATED_CDS.
 DR EMBL; L11064; G348247; -;
 DR EMBL; S65335; G442326; -;
 DR EMBL; S66181; G435782; -;
 DR PIR; S37807; S37807.
 DR PIR; B48227; B48227.
 DR GCRDB; GCR_0229; -;
 DR GCRDB; GCR_0493; -;
 DR GCRDB; GCR_0634; -;


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DR GCRDB: GCR_0842: -.
DR MGD: MGI:97438: OPRD1.
DR PROSITE: PS00237: G-PROTEIN_RECEPTOR; 1.
DR PFAM: PF00001; 7tm_1; 1.
DR K W G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT DOMAIN 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT DOMAIN 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372
FT CARBOHYD 18
FT CARBOHYD 33
FT DISULFID 121
FT LIPID 333
SQ SEQUENCE 372 AA; 40561 MW; 514022F5 CRC32;

Query Match 56.3%; Score 1597; DB 1; Length 372;
Best Local Similarity 66.7%; Pred. No. 1.62e-291;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;

Db 47 ALAATAIYSAVCAVGLLGNVLNMGIVKTKLATNIXIFNLALADALATSLPQOS 106
Qy :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
57 AIPVITAVISVVFVVGVLNGLSNVFIIRYTKMTATNIYIFNLALADALATVITMPQS 116
Db 107 AKYLMETPFGEELCKAVLSIDYNNMFTSIFTLTMMSDVRYIAVCHPVKALDFRIPAKAK 166
Qy :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
117 AVYLMNSPFGDLVCKIVISIDYNNMFTSIFTLTMMSDVRYIAVCHPVKALDFRIPAKAK 176
Db 167 LINICIWLAGSVPIWMAVTPRDGA-VV-CMLQFSP--SNYWDVTVKICVFLFAF 222
Qy :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
177 IINICIWLLASSVGSIAIVLGKTKREDVDVIECSLQFPDDDEYSW-WDLFMKICVFEAF 235
Db 223 VVPIIILVCYGLMLRLRSYVLLSGSKESLRIRIEMVLVYVGAFCVWCAPIHIVI 282
Qy :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
236 VIPVILIIIVCTMLIRLSKVLKLSGSKREKDNRIIRKLVLVVAVFIICTWPIIHIFIL 295
Db 283 VVTLVDINRDPVVAALHLCIALGYANSSLPVLYAFIDENFKRCFRQLCRTCPCGROBP 342
Qy :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
296 VEALGSTSHSWA-ALSSYFICIALGYTNSSLPVLYAFIDENFKRCFRDCEFPKRMWR 354
Db 343 GSLRRPRA 351
Qy :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
355 QSTNEVRNT 363

RESULT 13
ID OPX_RAT STANDARD; PRT; 367 AA.
AC P35370;
DI 01-JUN-1994 (REL. 29, CREATED)
DI 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DI 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (KOR-3) (FOR-C) (XOR1).
GN OPR11 OR OOR.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISLAR; TISSUE=BRAIN;
RX MEDLINE; 94215703.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESEIWA H., IWABE N.,

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RA MIYAJA T., HOUTANI T., SUGIMOTO I.;
RT "cDNA cloning and regional distribution of a novel member of the
RL opiod receptor family.";
RN FEBS LETT. 343:42-46(1994).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RA MENG F., XIE G., ALFRED M., THOMPSON R., HOVERSTEN M., WATSON S.,
RA AKIL H.;
RN SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA MEDLINE; 94307401.
RX BUNZOW J.R., SAEZ C., MORTUUD M., BOUVIER C., WILLIAMS J.T., LOW M.,
RA GRANDY D.K.;
RT "Molecular cloning and tissue distribution of a putative member of
the rat opiod receptor gene family that is not a mu, delta or kappa
opioid receptor type.";
RL FEBS LETT. 347:284-288(1994).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94307400.
RA CHEN Y., FAN Y., LIU J., MESTEK A., TIAN M., KOZAK C.A., YU L.;
RT "Molecular cloning, tissue distribution and chromosomal localization
of a novel member of the opiod receptor gene family.";
RL FEBS LETT. 347:279-283(1994).
[5]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 95096849.
RA LACHOWICZ J.E., SHEN Y., MONSMA F.J. JR., SIBLEY D.R.;
RT "Molecular cloning of a novel G protein-coupled receptor related to
the opiate receptor family.";
RL J. NEUROCHEM. 64:34-40(1995).
[6]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94298959.
RA WANG J.B., JOHNSON P.S., IMAI Y., PERSICO A.M., OZENBERGER B.A.,
RA EPPLER C.M., UHL G.R.;
RT "cDNA cloning of an orphan opiate receptor gene family member and its
splice variant.";
RL FEBS LETT. 348:75-79(1994).
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 95182817.
RA WICK M.J., MENNERATH S.R., LIN X., ELDE R.P., LAW P.Y., LOH H.H.;
RT "Isolation of a novel cDNA encoding a putative membrane receptor with
high homology to the cloned mu, delta, and kappa opiod receptors.";
RL BRAIN RES. MOL. BRAIN RES. 27:37-44(1994).
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLIL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D16438; G533355; -
DR EMBL; U05239; G451844; -
DR EMBL; U01913; G487965; -
DR EMBL; L28144; G496220; -

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DR EMBL; U07871; G606803; -
DR EMBL; L33916; G557200; -
DR EMBL; L29419; G510719; -
DR PIR; S46238; S46238.
DR PIR; S43655; S43655.
DR GCRDB; GCR_0834; -
DR GCRDB; GCR_0898; -
DR GCRDB; GCR_0912; -
DR GCRDB; GCR_1030; -
DR GCRDB; GCR_1455; -
DR GCRDB; GCR_1487; -
DR GCRDB; GCR_1517; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
DR HSPSP; P34996; 1DDD.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 84
FT TRANSMEM 85 106
FT DOMAIN 107 121
FT TRANSMEM 122 143
FT DOMAIN 144 162
FT TRANSMEM 163 185
FT DOMAIN 186 208
FT TRANSMEM 209 233
FT DOMAIN 234 261
FT TRANSMEM 262 285
FT DOMAIN 286 297
FT TRANSMEM 298 319
FT DOMAIN 320 366
FT DISULFID 120 197
FT LIPID 331 331
FT CARBOHYD 21 21
FT CARBOHYD 26 26
FT CARBOHYD 36 36
FT CONFLICT 105 105
FT CONFLICT 226 226
FT CONFLICT 246 246
FT CONFLICT 348 348
SQ SEQUENCE 367 AA; 40523 MW; 7FD40CCC CRC32;

Query Match 51.9%; Score 1473; DB 1; Length 367;
Best Local Similarity 59.3%; Pred. No. 7.03e-266;
Matches 188; Conservative 63; Mismatches 6; Indels 5; Gaps 5;

Db 40 SAFLPLGLKVTIVGLYLAVCIGLGLGNCIVMYVILRHMKTKATNIYIFNLALADTLVLL 99
Qy 51 SAHISPAIVITAVYSVVFVGLVGNLSVMEVITRYKMKTKATNIYIFNLALADALVTT 110

Db 100 TLFFGCTDILLGFNGNALKVTIAIDYNNFTFTFLIANSVDYVAICHPRALDVR 159
Qy 111 TPFQSAVYLMNSWPFQGVLCIKVISIDYNNFTFTFTIIMNSVDYVAICHPVKAOLF 170

Db 160 TSSKAQVNVATWALASVGVVPAVMGSAQV-EDDEE-IECLVEIPADQY-WGPVFA-IC 215
Qy 171 TEKKAKINICILWASSVGSIAVIGTKVREDVDVIECSLQFPD-DEYSWDFLMKIC 229

Db 216 IFLFIFLPLVLIISYCSILMIRRLRGVRLLSGSRKDRNLRRITRLVLVVAFFVGCWTP 275
Qy 230 VFVEAFVPLVLIIVCYITLMILRLKASVRLSGSRKDRNLRRITKLVLVVAFFIICWTP 289

Db 276 VGVFVLVGLGVQSGPFAVAILRCTLGALGYVNSCLNFIYAFIDENKACPKRKCASS 335
Qy 290 THIFTLVAGLSTSTAALSSYVEFCIALGYTNSSLNFLVAFIDENKACPKRKCFCFTK 349

Db 336 LHREMQVSDVRYSIAKD 352
Qy 350 MMEKQSTNVRNTVQD 366

RESULT 14
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Db      43 GAFLPLGLKVTIGLYLAVCVGGILGNCLPMYVILRHTKMKTATNIYIFNLALASTLVLL 102
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QY 51 SAHSPAPVITITAVYSVFVGVGNSLVMEFVIRITKKTATNIYIFNLALADALVTT 110
Db 103 TLPEQGTIDILGFWPFGNALCKTVIAIDYNNMFTSTFILTAMSVDRYVAICHPIRALDVR 162
QY 111 TMPTQSAVYLNNSWPFQGVLCCKIVISIDYNNMFTSIFTLTWMSVDRYIAVCHPVKALDFR 170
Db 163 TSSKAQAVNVAIWALASVGVVPVAIMSAQY-EDDE-IECLVEIPTQDY-WGPVFA-IC 218
QY 171 TPLKAKIINICIMLLASSVGSIAVLGGTKYREDVDVIECSLQFPD-DEYSWMDLFMKIC 229
Db 219 IFLESFIVPVLVIVSVCYSLMIRRLRGVRLSGSREKDRNLRRITRLVLVYVAVFVGWTP 278
QY 230 VFVFAFVLPVLLIIVCYITMILRLKSVRLSGSREKDRNLRRITRLVLVYVAVFIICTWP 289
Db 279 VQVFLAQGLGVQPSSEFAVAILRFCTALGYVNSCLNPILYAFLDENFKACFRKFCOCASA 338
QY 290 IHIFILVEALGSTSHSTAALSSYFFCIAIGYTNSSLNPNVLYAFLDENFKRCFRDFCFPIK 349
Db 339 LRRDVQVSDRVRSIAKDVA 357
QY 350 MRMERQSTNRVNTVQDPA 368

Search completed: Thu Feb 17 11:13:17 2000
Job time : 16 secs.

WQREH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Feb 17 11:13:35 2000; Maspar time 27.84 Seconds
Tabular output not generated. 745.004 Million cell updates/sec

Title: >US-08-455-683-2
Description: (1-380) from US08455683.pep
Perfect Score: 2839
Sequence: 1 MESPIOIFRGDPGPTCPSA.....RNTVQDPASMDYGGMKNKP 350

Scoring table: PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl9
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 48.857; Variance 122.078; scale 0.400

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	1687	59.4	373 13	OPIOID RECEPTOR HOMO	1.07e-252
2	1652	58.2	383 13	MU-OPIOID RECEPTOR.	8.81e-247
3	860	30.3	117 11	OPIOID RECEPTOR, KAPPA	2.26e-114
4	662	23.3	119 11	DELTA OPIOID RECEPTOR/	4.68e-82
5	613	21.6	371 11	GALANIN RECEPTOR TYPE	3.70e-74
6	610	21.5	387 4	GALANIN RECEPTOR GALR2	1.12e-73
7	595	21.0	353 13	CXCR4.	2.87e-71
8	588	20.7	352 6	CHEMOKINE RECEPTOR CCR	3.79e-70
9	576	20.3	352 6	CCR5 RECEPTOR (FRAGMENT)	3.16e-68
10	575	20.3	352 4	CCR5 RECEPTOR (FRAGMENT)	4.56e-68
11	572	20.1	359 11	RECEPTOR PROTEIN CCR3.	1.38e-67
12	569	20.0	383 14	G PROTEIN-COUPLED RECE	4.15e-67
13	564	19.9	352 6	CCR5 RECEPTOR (FRAGMENT)	2.61e-66
14	565	19.9	359 11	CHEMOKINE RECEPTOR CCR	1.81e-66
15	563	19.8	352 6	CCR5 RECEPTOR (FRAGMENT)	3.77e-66
16	547	19.3	374 13	G PROTEIN COUPLED P2Y	1.34e-63
17	545	19.2	357 13	CXC CHEMOKINE RECEPTOR	2.78e-63
18	535	18.8	360 6	CHEMOKINE RECEPTOR.	1.08e-61
19	532	18.7	353 13	MESSENGER-ASSOCIATED	3.24e-61
20	532	18.7	373 11	CHEMOKINE RECEPTOR CCR	3.24e-61

21	527	18.6	465 5	044426	CARDIOEXCITATORY RECP	2.01e-60
22	519	18.3	344 6	077833	CHEMOKINE RECEPTOR CCR	3.79e-59
23	513	18.1	263 5	076873	EG:121E7.2 PROTEIN.	3.32e-58
24	515	18.1	333 4	014694	CCR5 RECEPTOR (FRAGMENT)	1.60e-58
25	514	18.1	361 11	035811	G-PROTEIN COUPLED RECE	2.30e-57
26	505	17.8	370 4	075194	HUMAN PROLACTIN-RELEAS	6.10e-57
27	505	17.8	678 5	094736	TACHYKININ-LIKE RECEPT	6.10e-57
28	500	17.6	368 4	060755	GALANIN 2 RECEPTOR HOM	3.76e-56
29	488	17.2	367 11	054689	G PROTEIN-COUPLED RECE	2.92e-54
30	489	17.2	370 11	088853	GALANIN RECEPTOR TYPE	2.03e-54
31	486	17.1	370 4	015132	P2Y5-LIKE RECEPTOR.	6.03e-54
32	482	17.0	360 4	060835	CXCR4 GENE ENCODING RE	2.57e-53
33	483	17.0	370 11	088626	GALANIN RECEPTOR TYPE	1.79e-53
34	479	16.9	352 6	077488	CXCR4 RECEPTOR.	7.60e-53
35	481	16.9	372 13	093237	CXC CHEMOKINE RECEPTOR	3.69e-53
36	476	16.8	303 13	P70058	ANGIOTENSIN RECEPTOR R	2.25e-52
37	477	16.8	429 5	P92045	LYMNOKININ RECEPTOR.	1.57e-52
38	465	16.4	370 11	054914	GALANIN RECEPTOR TYPE	1.19e-50
39	464	16.3	399 11	089790	BOMBESIN RECEPTOR SUBT	1.71e-50
40	463	16.3	399 11	054798	BOMBESIN-LIKE RECEPTOR	2.45e-50
41	451	15.9	168 11	035715	SOMATOSTATIN RECEPTOR	1.84e-48
42	449	15.8	378 11	008707	CHEMOKINE (C-C) RECEPT	3.78e-48
43	447	15.7	390 11	054799	NEUROMEDIN B RECEPTOR	7.74e-48
44	442	15.6	238 13	Q92158	ANGIOTENSIN II RECEPTO	4.66e-47
45	438	15.4	343 11	088537	N-FORMYLPEPTIDE RECEPT	1.95e-46

ALIGNMENTS

RESULT 1
ID O57585 PRELIMINARY; PRG: 373 AA.
AC O57585;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE OPIOID RECEPTOR HOMOLOGUE.
OS BRACHYDANTIO RERIC (ZEBRAFISH) (ZEBRA DANIO).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
OC CYPRINIDAE; RASBORINAE; DANIO.
RN [1]
RP SEQUENCE FROM N.A.
RA BARRALLO A., GONZALEZ-SARMIENTO R., GARCIA-MALVAR F., RODRIGUEZ R.E.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AJ001596; E1217986; -
DR PROSITE; PS00237; G-PROTEIN-RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 373 AA; 42520 MW; E900D477 CRC32;

Query Match 59.4%; Score 1687; DB 13; Length 373;
Best Local Similarity 65.6%; Pred. No. 1.07e-252;
Matches 206; Conservative 62; Mismatches 42; Indels 4; Gaps 4;

Db	51	IAISITATSYVYCVVGLGNILVMGVVRYNKLKATNYIFNLALADALATSTLP	110
Qy	58	IPVITATSYVYVGLVGNLSLMEVIRYTKTKATNYIFNLALADALVTTMPF	117
Db	111	KYLMNTWPFGLCKVVAIDYNNFTSIFTITMMSVDRIYAVCHPVRALEFRPI	170
Qy	118	VYLMNSWPFGLVCKIVSIDYNNFTSIFTITMMSVDRIYAVCHPVKALDFRPL	177
Db	171	INVCIIWISSAVGVDIMVAVRTVNTQNTV-CMLKFPDPDW-YWDVTVKTCVFI	228
Qy	178	INICIIWISSAVGVDIMVAVRTVNTQNTV-CMLKFPDPDW-YWDVTVKTCVFI	237
Db	229	PVYIIICVGLMILKSVRLSSKEDRNKRITRNVVAVAFICWTPIHFIIEK	288
Qy	236	PVLIIVCYTLMILKSVRLSSKEDRNKRITRNVVAVAFICWTPIHFIIEK	297
Db	289	IVTDINKNPFIASWHLRT-GYTNSSLNPLVAFIDENKRCFRDCLPFRADQSN	347
Qy	296	ALGSTSHSTA-ALSIYFICIALGYTNSSLNPLVAFIDENKRCFRDCLPFRADQSN	356

IDENTIA;


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QY 212 LQFP--DDEYSWDLFMKICVFAEVPVLIIVCYTLMILRLKSVRLSGSREKDRNL 270
AC 077776; PRELIMINARY; PRT; 352 AA.
RA CHEN Z., KWON D., JIN Z., MONARD S., TELFER P., JONES M., LU C.,
RA AGUIAR R., HO D.D., MARX P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
RL with a R2b-tropic simian immunodeficiency virus.";
RI J. EXP. MED. 0:0-0(1998).
DR EMBL; AF084004; G3694849; -.
SQ SEQUENCE 352 AA; 40475 MW; 6649F573 CRC32;

Query Match 20.7%; Score 588; DB 6; Length 352;
Best Local Similarity 29.6%; Pred. No. 3.79e-70;
Matches 89; Conservative 98; Mismatches 98; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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RESULT 8
ID 077776; PRELIMINARY; PRT; 352 AA.
AC 077776;
RA CHEN Z., KWON D., JIN Z., MONARD S., TELFER P., JONES M., LU C.,
RA AGUIAR R., HO D.D., MARX P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
RL with a R2b-tropic simian immunodeficiency virus.";
RI J. EXP. MED. 0:0-0(1998).
DR EMBL; AF084004; G3694849; -.
SQ SEQUENCE 352 AA; 40475 MW; 6649F573 CRC32;

Query Match 20.7%; Score 588; DB 6; Length 352;
Best Local Similarity 29.6%; Pred. No. 3.79e-70;
Matches 89; Conservative 98; Mismatches 98; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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RESULT 9
ID 018770; PRELIMINARY; PRT; 352 AA.
AC 018770;
RA CHEN Z., KWON D., JIN Z., MONARD S., TELFER P., JONES M., LU C.,
RA AGUIAR R., HO D.D., MARX P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
RL with a R2b-tropic simian immunodeficiency virus.";
RI J. EXP. MED. 0:0-0(1998).
DR EMBL; AF084004; G3694849; -.
SQ SEQUENCE 352 AA; 40475 MW; 6649F573 CRC32;

Query Match 20.7%; Score 588; DB 6; Length 352;
Best Local Similarity 29.6%; Pred. No. 3.79e-70;
Matches 89; Conservative 98; Mismatches 98; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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OC CATARRHINI; HOMINIDAE; PAN.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MACR5-140A;
RA ZHANG L., CARUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR EMBL; AF011538; G2305194; -.
DR PFAM; PF00001; 7tm_1; 1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40523 MW; F1C10E99 CRC32;

Query Match 20.3%; Score 576; DB 5; Length 352;
Best Local Similarity 29.2%; Pred. No. 3.16e-68;
Matches 88; Conservative 98; Mismatches 99; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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RESULT 10
ID 015538; PRELIMINARY; PRT; 352 AA.
AC 015538;
RA CHEN Z., KWON D., JIN Z., MONARD S., TELFER P., JONES M., LU C.,
RA AGUIAR R., HO D.D., MARX P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
RL with a R2b-tropic simian immunodeficiency virus.";
RI J. EXP. MED. 0:0-0(1998).
DR EMBL; AF011536; G2305190; -.
DR PFAM; PF00001; 7tm_1; 1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40552 MW; BLECA8D9 CRC32;

Query Match 20.3%; Score 575; DB 4; Length 352;
Best Local Similarity 28.9%; Pred. No. 4.56e-68;
Matches 87; Conservative 100; Mismatches 98; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR EMBL; AF011536; G2305190; -.
DR EMBL; AF011516; G2305150; -.
DR EMBL; AF011534; G2305186; -.
DR PFAM; PF00001; 7tm_1; 1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40552 MW; BLECA8D9 CRC32;

Query Match 20.3%; Score 575; DB 4; Length 352;
Best Local Similarity 28.9%; Pred. No. 4.56e-68;
Matches 87; Conservative 100; Mismatches 98; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR EMBL; AF011536; G2305190; -.
DR EMBL; AF011516; G2305150; -.
DR EMBL; AF011534; G2305186; -.
DR PFAM; PF00001; 7tm_1; 1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40552 MW; BLECA8D9 CRC32;

Query Match 20.3%; Score 575; DB 4; Length 352;
Best Local Similarity 28.9%; Pred. No. 4.56e-68;
Matches 87; Conservative 100; Mismatches 98; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR EMBL; AF011536; G2305190; -.
DR EMBL; AF011516; G2305150; -.
DR EMBL; AF011534; G2305186; -.
DR PFAM; PF00001; 7tm_1; 1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40552 MW; BLECA8D9 CRC32;

Query Match 20.3%; Score 575; DB 4; Length 352;
Best Local Similarity 28.9%; Pred. No. 4.56e-68;
Matches 87; Conservative 100; Mismatches 98; Indels 16; Gaps 14;

Db 21 QKINVKQIAARLLPPLYSLVFVFGVGNILVLIILNCKRLKSMTDIYLLNLAISDLFL 80
QY 50 ESAHISPAIPVITAVSYVFGVGNLSVFMFVIIRYTKMTATNIYIFNLADALVT 109
Db 81 LVVPF-WAHYAAQWDFGNTMQLLGLYFIFGFSGIFFIILLTIDRYLAIVHAFALKA 139
QY 110 TTFQSAVILMNSWPFGLVCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDF 169
Db 140 RVTFGVTSVITWVAVFASLPGLIFTRSQ-REGHYT-CSPHPYSQYQWKNFQTLK 197
QY 170 RPLKAKINICIWLLASVGSISAVILGKTKYREDVDVIECSLQFPDDYSWDLFMKIC 229
Db 198 IYVILGLVPLLVVICYS-GIL-KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP 250
QY 230 VFVFAFVPLVLIIVCYTLMILRLKSVRLSGSREKDRNLRIITKLVVAVVFIICWTP 289
Db 251 YNIVLLNTFQFFGLNCSNRLDQAMQVETLGMHCCINPIIYAFVGEKFRNYLV 310
QY 290 IHI-FIL-V-EAL-G-STSHSTAALS-SYFICIALGYTNSLNPVLYAFDENFKRCFRD 343
Db 311 F 311
QY 344 F 344

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Db      40  LLPLSLVPIFVIGLGNMVMVLIIKYKRLQIMNTYILNLALSULLFTVPF-WIHVV 98
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61  IITAVSVFWVGSGNSLMKFVIIRYIKMTATNIYFNLAADALVTMPFQSAYVL 120
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      99  LKNWEGFGHCKMKSLGXYLYALYSIEFFIILTIDRYLAIVHAVALARARTVPTAITS 158
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     121  M-NSWFPGDVLCRAVISIDYNNMFTSIFLTMMSDVRYIAVCPVKALDFRPLAKIIN 179
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     159  IITWGIAVLAALPEFPHGS-QDNFGDI.SCSPRYPEGEDSNKREHALRMIFGLAPEL 216
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     180  ICITWLLASSGISAIVLGGTKVEDVDVIECSLQFPDEVSWMDLFMKICVFVAEVIPV 239
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     217  LIMVICYS-GII--KT--LLR-CPNKKKH-KAT-QLTFVVMIVVEFTWPYNLVLLLSAF 268
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     240  LIIVCYTLMILRKSVRLSSGREKDRNURRTKLIVVVAVFICTWPIH-IPFL-V- 296
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     269  HSTLETSCQSHLDIAMOVTEVITHCCINPIIFYAFGERFRKHLRF 319
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     297  EA-LGSTSHSTAALS-SYYFCIALGVNTSSNPVLYAFIDENFKCFRDE 344
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
ID      Q89609          PRELIMINARY;           PRT;       383 AA.
AC      Q89609;
DT      01-NOV-1996 (1, CREATED)
DT      01-NOV-1996 (TREMBREL 01, LAST SEQUENCE UPDATE)
DT      01-NOV-1998 (TREMBREL 08, LAST ANNOTATION UPDATE)
DE      G PROTEIN-COUPLED RECEPTOR.
OS      EQUINE HERPESVIRUS TYPE 2 (EHV-2).
OC      VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
OC      BETAHERPESVIRINAE.
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RESULT      13
ID          Q18772      PRELIMINARY;      PRT;      352 AA.
AC          Q18772;
DT          01-JAN-1998 (IREMREL. 05, CREATED)
DT          01-JAN-1998 (IREMREL. 05, LAST SEQUENCE UPDATE)
DT          01-NOV-1998 (IREMREL. 08, LAST ANNOTATION UPDATE)
DE          CCR5 RECEPTOR (FRAGMENT).
GN          CCR5.
OS          PAN TROGLODYTES (CHIMPANZEE).
OC          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
NC          CATARRHINI; HOMINIDAE; PAN.
RC          [1]
RP          SEQUENCE FROM N.A.
RA          STRAIN=CHCGR5-1428;
CA          ZHANG L., CARROTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
HO          D.D.;
RL          AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR          ENBL; AF011541; G2305200; -.
RF          PF00001; 7tm_1; 1.
FT          NON_TER      352      352.
SQ          SEQUENCE      352 AA;      40598 MW;      A9BF8EDF CRC32;

Query Match      19.9%;      Score 564;      DB 6;      Length 352;
Best Local Similarity      28.2%;      Pred. No. 2,61e-66;
Matches      85;      Conservative 100;      Mismatches 100;      Indels 16;      Gaps 14;

Db      21 QKINVQIARLLPPYLSLVFTGFDNMVLIVILLINCARKLSMTDIYLNLIAISDLFL 80
       :      :      :      :      :      :      :      :      :      :      :      :      :      :      :      :
QY      50 ESASIPAEPIITAVSYVVFVGLVGNLSLMVFILRYTKMKIATNIYIFNLALADALVT 109
       :      :      :      :      :      :      :      :      :      :      :      :      :      :      :      :

Db      81 LTVPF-WAHYAAAQWDFGMTMCOLLTGLYFIQFFSGIFFIIILTIDRYLAIVHAFKA 139

```

QY	110	TTMPFQSAVYLMNSWPFQDVLCKIVISIDYNNFTSLFTITMMSVDRIYAVCHPVKALDF	169
Db	140	RTVTEGVTGVTWVAVFASLPGIITFRSQ-KEGLHYT--CSSHFYSQYQWKNFQILK	197
QY	170	RTPLKAKIINCITWLIASSVGISAIVLGGTKVEDVDVIECSLOFPDDEYSWWDLFMKIC	229
Db	198	IVILGLVPLLVWVICS-GIL--KT--LLRCNKKRH-RAY-RIIFTIMIVYFLWAP	250
QY	230	VFPAPFVPIVLIITVCYITLMLRKSVRLSSGREKDRNLRTTKIVLVVVAVFIICWIP	289
Db	251	YDIYLLANTQEFGLNCCSSNRLDQAMQVTELTGTHCCINPIIYAFVGEKERNVLLV	310
QY	290	IHI-FIL-V-EAL-G-STSHSTAALS-SYFPCIALGTNSLAPVIAFDENKRCFRD	343
Db	311	F 311	
QY	344	F 344	
RESULT 14			
ID	Q54814	PRELIMINARY; PET; 359 AA.	
AC	Q54814;		
DT	01-JUN-1998 (TREMBLREL. 06, CREATED)		
DT	01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
DE	CHEMOKINE RECEPTOR CCR3.		
OS	EUTAKU NORVEGICUS (RAI).		
OC	REKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;		
RC	CSUIROGNATHI; MURIDAE; MURINAE; RATTUS.		
RC	[1]		
RP	SEQUENCE FROM N. A.		
RC	STRAIN-WISTAR; TISSUE-SPLEEN;		
RA	JIANG Y., SALAFRANCA M.N., ADHIKARI S., XIA Y., FENG L., SONNTAG M.K.,		
RA	DEFIBRE C.M., PENNELL N.A., STREET W.J., HARRISON J.K.;		
RL	J. NEUROIMMUNOL. 0:0-0(1998).		
DR	ENBL: AF003954; G2897073; -		
SQ	SEQUENCE 359 AA; 41643 MW; CLFC70CA CRC32;		
Query Match 19.9%; Score 565; DB 11; Length 359;			
Best Local Similarity 30.9%; Pred. No. 1.81e-66;			
Matches 90; Conservative 93; Mismatches 90; Indels 18; Gaps 14;			
Db	40	LLPLYSIAVFTVGLGNMVMVLLIKYRKIQIMTNIYLLNLAISDLFLTFIVFP-WIHVY 98	
QY	61	LIIVAVSVFVGLVGNLSVMFVIIRTKKATNIYFNLAADALVTITMFPQSAVL 120	
Db	99	LWNWEGFGHCCKMKSGLIYALYSEIFFILLTIDRYLAIVHAVLALRARITVTFATIS 158	
QY	121	M-NSWPFQDVLCKIVISIDYNNFTSIFTITMMSVDRIYAVCHPVKALDFRTPLKAKIIN 179	
Db	159	IITWGFVAFLAALPFEIHES--QDNFGDLSCSPRYPEGEEDSKRPHALRMNTFGLALPL 216	
QY	180	ICIWLLASSVGISAIVLGGTKVEDVDVIECSLOFPDDEYSWWDLFMKICVFVFAVPIV 239	
Db	217	LIWVICS-GII--KT--LLR-CENKKH-KAI-QLIFVVMIVFFFTWFTVNYVLLLSAF 268	
QY	240	LIIVCVTILMLRKSVPLSSGREKDRNLRTTKIVLVVVAVFIICWPIH-IFIL-V- 296	
Db	269	HSTFLETSCQOISHLDLAMQVTEVITHTHCCINPIIYAFVGERFRKHLRLF 319	
QY	297	EA--LGSTSHSTAALS-SYFPCIALGTNSLAPVIAFDENKRCFRD 344	

[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2000, 10:09:49 ; Search time 1154.67 Seconds
(without alignments)
-2629.655 Million cell updates/sec

Title: US-08-455-683-11
Perfect score: 1000
Sequence: 1 AAGAGCAAAATCAGTAATC.....CCAGTATGACTAGTCGTGGA 1000

Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl.*

Word size : 0

Number of hits that pass the threshold : 1642386

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pl3.*
- 10: gb_pr2.*
- 11: gb_pr3.*
- 12: gb_ro.*
- 13: gb_sts.*
- 14: gb_sy.*
- 15: gb_un.*
- 16: gb_vl.*
- 17: em_fun.*
- 18: em_hum1.*
- 19: em_hum2.*
- 20: em_in.*
- 21: em_om.*
- 22: em_or.*
- 23: em_ov.*
- 24: em_pat.*
- 25: em_ph.*
- 26: em_pl.*
- 27: em_ro.*
- 28: em_sts.*
- 29: em_sy.*
- 30: em_un.*
- 31: em_vl.*
- 32: gb_htg1.*
- 33: gb_htg2.*
- 34: gb_in1.*
- 35: gb_in2.*
- 36: gb_ba1.*
- 37: em_ba2.*
- 38: em_hum3.*
- 39: em_hum4.*
- 40: gb_pr4.*
- 41: gb_htg3.*
- 42: gb_htg4.*
- 43: gb_htg5.*
- 44: gb_htg6.*
- 45: gb_htg7.*
- 46: em_htg1.*
- 47: em_htg2.*
- 48: em_htg3.*
- 49: em_hum5.*

50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	455	45.5	455	9	HUMOPRK1A	L36079 Homo sapien
2	439	43.9	1142	5	A48343	A48343 Sequence 1
3	439	43.9	1604	9	HUMOPRK1B	L37362 Homo sapien
4	439	43.9	1154	11	HSU17298	U17298 Human kappa
5	354	35.4	1182	9	HSU11053	U11053 Human kappa
6	252	25.2	183559	42	AC009646	AC009646 Homo sapi
7	221	22.1	1229	9	HSU16860	U16860 Human kappa
8	196	19.6	432	9	HUMKOR	L36130 Homo sapien
9	47	4.7	1733	12	CPU04092	U04092 Cavia porce
10	41	4.1	715	3	AF012105	AF012105 Sus scrof
11	33	3.3	432	12	MMU16998	U16998 Mus musculu
12	33	3.3	488	12	MUSMORGDP2	D31664 Mouse MORG
13	33	3.3	658	12	RNKOR2	U17994 Rattus norv
14	33	3.3	1109	12	S77868S2	S77869 kappa opioi
15	32	3.2	1408	5	A68828	A68828 Sequence 5
16	32	3.2	2481	5	E08874	E08874 cDNA coding
17	32	3.2	1410	12	MUSKAPOPRE	L11065 Mouse kappa
18	32	3.2	2481	12	RATKOR	D16829 Rattus norv
19	32	3.2	1359	12	RATKOR1A	L22001 Rat kappa o
20	32	3.2	2094	12	RATKOR1B	L22536 Rattus norv
21	32	3.2	1273	12	RATROD	D16534 Rat mRNA fo
22	32	3.2	4048	12	RNKOR3	U17995 Rattus norv
23	32	3.2	4742	12	RNU00442	U00442 Rattus norv
24	32	3.2	1288	12	S81111	S81111 kappa-opioi
25	29	2.9	686	3	SSU71149	U71149 Sus scrofa
26	29	2.9	2219	5	A38528	A38528 Sequence 1
27	29	2.9	2218	5	A68826	A68826 Sequence 3
28	29	2.9	2272	12	MUSDELOPRE	L11064 Mouse delta
29	29	2.9	2219	12	MUSDELTO	L06322 Mus musculu
30	29	2.9	1835	12	MUSDOPRC	L07271 Mouse delta
31	29	2.9	1418	12	RATROA	D16348 Rat mRNA no
32	29	2.9	1366	12	RNU00475	U00475 Rattus norv
33	29	2.9	1834	12	S65335	S65335 delta opioi
34	29	2.9	2203	12	S66181	S66181 delta opiat
35	29	2.9	356	12	S81965	S81965 delta opioi
36	26	2.6	638	12	MUSMORGDP3	D31665 Mouse MORG
37	26	2.6	1401	12	RATMPIOID	L22455 Rat mu opio
38	26	2.6	1586	12	RATMORA	L13069 Rattus norv
39	26	2.6	2135	12	RATMUORIA	L20684 Rattus norv
40	26	2.6	2397	12	RATROB	D16349 Rat mRNA fo
41	26	2.6	1448	12	RNU02083	U02083 Rattus norv
42	26	2.6	1367	12	RNU35424	U35424 Rattus norv
43	26	2.6	720	12	S77863	S77863 mu-opioi r
44	26	2.6	1186	12	S77868S3	S77872 kappa opioi
45	25	2.5	2162	9	HUMMOR1X	L25119 Human Mu op

ALIGNMENTS

RESULT	1	HUMOPRK1A	LOCUS	HUMOPRK1A	455 bp	DNA	PRI	07-JAN-1995
DEFINITION				Homo sapiens (clone hSR4-1) kappa opiod receptor (OPRK1) gene, complete exon.				
ACCESSION				L26079				
VERSION				L26079.1		GI:415143		
KEYWORDS				OPRK1 gene; kappa opiod receptor.				
SOURCE				Homo sapiens (tissue library: Stratagene 946203; placenta DNA.				
ORGANISM				Homo sapiens				
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				

REFERENCE 1 (bases 1 to 455)
AUTHORS Yasuda,K., Espinosa,R.III., Takeda,J., Le Beau,M.M. and Bell,G.I.
TITLE Localization of kappa opioid receptor gene to human chromosome band 8q11.2
JOURNAL Unpublished (1994)
FEATURES Location/Qualifiers
source 1..455

organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="male"
/tissue_type="placenta"
/tissue_lib="Stratagene 946203; lambda"
/map="8q11.2"
101..453
/gene="OPRK1"
101..453
/gene="OPRK1"
/note="G00-132-651"
BASE COUNT 125 a 104 c 96 g 130 t
ORIGIN

Query Match 45.5%; Score 455; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 3.9e-246; Mismatches 0; Indels 0; Gaps 0;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGCAAAATCAGTAATCCAAAGCGTATCACAAACATTCACCTATGCGGTTTGAC 60
DB 1 AAGAGCAAAATCAGTAATCCAAAGCGTATCACAAACATTCACCTATGCGGTTTGAC 60
QY 61 TTGAAATGGAGGAAATGCTATTGTTCTTTCTTTTAGATACACAAAGATGAGACAG 120
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QY 361 TGAAGCAAAAGATCATCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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QY 421 CAATAGTCTTGGAGCCACCAAGTCAGGGAAGT 455
DB 421 CAATAGTCTTGGAGCCACCAAGTCAGGGAAGT 455

RESULT 2
A48343 1142 bp DNA PAT 07-MAR-1997
LOCUS A48343
DEFINITION Sequence 1 from Patent WO9601898.
ACCESSION A48343
VERSION A48343.1 GI:2302133
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1142)
AUTHORS Kieffer,B. and Simonin,F.
TITLE HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF

JOURNAL Patent: WO 9601898-A 1 25-JAN-1996;
UNIV PASTEUR (FR)
COMMENT Other publication FR 2722209 960112.
FEATURES Location/Qualifiers
source 1..1142

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BASE COUNT 236 a 337 c 283 g 286 t
ORIGIN

Query Match 43.9%; Score 439; DB 5; Length 1142;
Best Local Similarity 99.1%; Pred. No. 4.5e-237; Mismatches 7; Indels 0; Gaps 0;
Matches 789; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 160 CTTTGTGTACTACACCATGCGCTTTACAGAGTACGGTCTACTTGTGATTAATTCCTGGCCTT 219
DB 317 CTTTGTGTACTACACCATGCGCTTTACAGAGTACGGTCTACTTGTGATTAATTCCTGGCCTT 376
QY 220 TTGGGAGTGTCTGTGCAAGTAGTAATTTCCATTTGATTACTACACATGTTCCACAGCA 279
DB 377 TTGGGAGTGTCTGTGCAAGTAGTAATTTCCATTTGATTACTACACATGTTCCACAGCA 436
QY 280 ICTTCACCTTGACCATGATGAGCGTGGACCGCTACATTCGCCGTGSCCACCCTGGAAGG 339
DB 437 ICTTCACCTTGACCATGATGAGCGTGGACCGCTACATTCGCCGTGSCCACCCTGGAAGG 496
QY 340 CTTTGGATTTCCGACACACCTTTGAAGGCAAGATCATCAATCTGTGATCTGGTCTGT 399
DB 497 CTTTGGATTTCCGACACACCTTTGAAGGCAAGATCATCAATCTGTGATCTGGTCTGT 556
QY 400 CGTCAICTGTGGCATCTCTGCAATAGTCCCTTGGAGGACCAAAAGTCAGGGAAGTGTG 459
DB 557 CGTCAICTGTGGCATCTCTGCAATAGTCCCTTGGAGGACCAAAAGTCAGGGAAGTGTG 616
QY 460 ATGTCAATGAGTGTCTTGGCATTCACGATTCACGATGATGACTACTCTGTGGACCTTTCA 519
DB 617 ATGTCAATGAGTGTCTTGGCATTCACGATTCACGATGATGACTACTCTGTGGACCTTTCA 676
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QY 640 ATNNCAACCTGCGTAGGATCACACAGATGAGTCTGGTGTGGTGGTGGTGGTGGTGGTGGT 699
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QY 700 GCTGGACTCCCATTCACATATTCATCTGTTGGAGGCTCTGGGAGACCTCCCAACAGCA 759
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QY 760 CAGCTGCTCTCTCCAGCTATTAATCTCTGATCGCTTGGCTTATACCAACAGTACGCTGA 819

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Db 977 ATCCCAATTCCTACGCTTCTTTGATGAAACCTCAAGCGGTTCCTCCGGAGCTTCTGCT 1036
QY 880 TTCCACTGAAGATGAG 895
Db 1037 TTCCACTGAAGATGAG 1052

RESULT 3
LOCUS HUMOPRX1B 1604 bp mRNA PRI 22-MAR-1995
DEFINITION Homo sapiens (clone d2-115) kappa opiod receptor (OPRX1) mRNA, complete cds.
ACCESSION L373562
VERSION L373562.1 GI:722617
KEYWORDS OPRX1 gene; kappa opiod receptor; opiod receptor.
SOURCE Homo sapiens (clone d2-115) (tissue library: genomic in lambda dash and cDNA in lambda ZAPII) fetus brain cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1604)
AUTHORS Zhu, J., Chen, C., Xue, J.-C., Kunapuli, S., Deriel, J.K. and Liu-Chen, L.-Y.
TITLE Cloning of a human kappa opiod receptor from the brain
JOURNAL Life Sci. 56, 201-207 (1995)
FEATURES
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BASE COUNT 307 a 483 c 440 g 374 t
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Best Local Similarity 99.1%; Pred. No. 4.6e-237;
Matches 789; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 100 GATACACAAGATGAGACAGCAACCAATTACATATTACCTGGCTTTGGCAGATG 159
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QY 160 CTTTAGTACTACACCAAGCCCTTCAGAGTACGGCTCTACTGTGATGAATTCCTGCGCTT 219
Db 694 CTTTAGTACTACACCAAGCCCTTCAGAGTACGGCTCTACTGTGATGAATTCCTGCGCTT 753
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Db 814 TCTTCCACTTGACCATGATGAGCGGTGAGCCGCTACATTCGCGTGTGCCACCCGCGTGAAGG 873
QY 340 CTTTGGACTTCGCGACACCCCTTGAAGGCAAGATCAATATCTCATCTGCTGCTGCT 399
Db 874 CTTTGGACTTCGCGACACCCCTTGAAGGCAAGATCAATATCTCATCTGCTGCTGCT 933
QY 400 CGTCATCTCTTGGCATCTCTGCAATAGTCTTGGAGGACCAAGATCAGGAGGTGTCG 459
Db 934 CGTCATCTCTTGGCATCTCTGCAATAGTCTTGGAGGACCAAGATCAGGAGGTGTCG 993
QY 460 ATGTATATGAGTGTGCTTGGAGTCTCCAGATGATGACTACTCTGCTGGTGGGACCTCTTCA 519
Db 994 ATGTATATGAGTGTGCTTGGAGTCTCCAGATGATGACTACTCTGCTGGTGGGACCTCTTCA 1053
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QY 580 ACACCTGATGATCTGCTGCTCTCAAGANNNGTCCGGCTCTCTTCTGCTCCCGAGAGAAAG 639
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QY 640 ATNNCAACTGCGTGTAGGATCACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
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Db 1234 GCTGACTCCCATTCACATATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1293
QY 760 CAGTCTCTCTCCAGCTATTACTTCTGATCGCTTAGCTTAGCTATATACCAACAGTAGCTGA 819
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QY 820 ATCCCATCTCTACGCCCTTCTTGATGAAACTTCAAGCGGTGTTTCCGGGACTTCTGCT 879
Db 1354 ATCCCATCTCTACGCCCTTCTTGATGAAACTTCAAGCGGTGTTTCCGGGACTTCTGCT 1413
QY 880 TTCCACTGAAGATGAG 895
Db 1414 TTCCACTGAAGATGAG 1429

RESULT 4
LOCUS HSU17298 1154 bp mRNA PRI 14-JUL-1995
DEFINITION Human kappa opiod Receptor (hKOR) mRNA, complete cds.
ACCESSION U17298
VERSION U17298.1 GI:596069
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1154)
AUTHORS Simonin, F., Gaveriaux-Ruff, C., Befort, K., Matthes, H., Launes, B., Michelletti, G., Mattei, M.G., Charron, G., Bloch, B. and Kieffer, B.
TITLE kappa-Opiod receptor in humans: cDNA and genomic cloning, chromosomal assignment, functional expression, pharmacology, and expression pattern in the central nervous system
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (15), 7006-7010 (1995)
MEDLINE 95350200
REFERENCE 2 (bases 1 to 1154)
AUTHORS Maussone, E., Bare, L. and Yang, D.
TITLE Isolation of a human kappa opiod receptor cDNA from placenta
JOURNAL Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)
MEDLINE 94338360
REFERENCE 3 (bases 1 to 1154)
AUTHORS Kieffer, B.

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Db 885 GATGATGACTACTCCTGGTGGGACCTCTTCATGAAGATCGCGTCT 931
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RESULT 10
AF012105 715 bp mRNA MAM 26-JAN-1999
LOCUS
DEFINITION Sus scrofa kappa opioid receptor mRNA, partial cds.
ACCESSION AF012105
VERSION AF012105.1 GI:4102307
KEYWORDS
SOURCE pig.
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Pampusch, M.S., Zilliox, M., Osinski, M.A., Brown, D.R. and
Murtough, M.P.
TITLE Distribution of delta and kappa opioid receptor mRNA in porcine
immune tissues
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 715)
AUTHORS Pampusch, M.S.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1997) Veterinary Pathobiology, University of
Minnesota, 1971 Commonwealth Ave, 205 Veterinary Science, St. Paul,
MN 55108, USA

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Db 343 GTCCATCATCATCGTCTGCTACACCTCATGATCCTGGG 383
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RESULT 11

MMU16998
LOCUS
DEFINITION Mus musculus kappa opioid receptor (oprkl) gene, partial cds.
ACCESSION U16998
VERSION U16998.1 GI:595936
KEYWORDS house mouse.
SOURCE
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Grandy, D.K.
TITLE Mapping of the human kappa opioid receptor gene to chromosome
8q11.2-q12; no evidence for multiple kappa opioid receptor genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 432)
AUTHORS Grandy, D.K.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1994) David K. Grandy, Vollum Institute, Oregon
Health Sciences, University, 3181 S.W. Sam Jackson Park Road,
Portland, OR 97201, USA

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BASE COUNT 114 a 92 c 85 g 141 t
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Db 336 ATAGTCTTGGAGGCACCAAGTCAGGAAGGT 368
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RESULT 12
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LOCUS
DEFINITION Mouse MORGP gene for kappa-opioid receptor, exon 2.
ACCESSION D31564
VERSION D31564.1 GI:643594
KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and
peptides-binding; transmembrane protein.
SEGMENT 2 of 3
SOURCE Mus musculus DNA, clone_lib:phage lambda fixII.
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 488)
Nishi, M., Takeshima, H., Mori, M., Nakagawara, K. and Takeuchi, T.

TITLE Structure and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opioid receptor homologue (MOR-C)
JOURNAL Biochem. Biophys. Res. Commun. 205 (2), 1353-1357 (1994)
MEDLINE 95100967
REFERENCE 2 (bases 1 to 488)
AUTHORS Takeshima,H.
JOURNAL Direct Submission
Takeshima, H. (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi
Takeshima, Tokyo Institute of Psychiatry, Department of
Neurochemistry, 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan
(Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
COMMENT Submitted (28-May-1994) to DDBJ by:
Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.
FEATURES
Source
Location/Qualifiers
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89..441
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 411 ATAGTCTTGGAGGCACCAAGTCAGGGAAGGT 443
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RESULT 13
RNKOR2 658 bp DNA ROD 24-MAR-1995
LOCUS Rattus norvegicus kappa opioid receptor gene, exon 3.
DEFINITION U17994
ACCESSION U17994
VERSION U17994.1 GI:727257
KEYWORDS
SEGMENT 2 of 3
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 658)
AUTHORS Yakovlev,A.G., Krueger,K.E. and Faden,A.I.
TITLE Structure and expression of a rat kappa opioid receptor gene
JOURNAL J. Biol. Chem. 270 (12), 6421-6424 (1995)
MEDLINE 95204422
REFERENCE 2 (bases 1 to 658)
AUTHORS Yakovlev,A.G.
JOURNAL Direct Submission
Submitted (02-DEC-1994) Alexander G. Yakovlev, Georgetown
University School of Medicine, Neurology, 3900 Reservoir Rd.,
Washington, DC 20007, USA
FEATURES
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Location/Qualifiers
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579..>658
/number=3
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 423 ATAGTCTTGGAGGCACCAAGTCAGGGAAGGT 455
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DB 548 ATAGTCTTGGAGGCACCAAGTCAGGGAAGGT 580
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RESULT 14
S77868S2 1109 bp DNA ROD 26-SEP-1995
LOCUS kappa opioid receptor [mice, genomic, 1109 nt, segment 2 of 3].
DEFINITION S77869
ACCESSION S77869
VERSION S77869.1 GI:998530
KEYWORDS 2 of 3
SEGMENT Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1109)
AUTHORS Liu,H.C., Lu,S., Angustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H.
and Wei,L.N.
TITLE Cloning and promoter mapping of mouse kappa opioid receptor gene
JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE 95251663
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 166534] from the original journal article.
This sequence comes from Fig. 2.

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BASE COUNT 331 a 213 c 204 g 361 t
ORIGIN

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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 423 ATAGTCTTGGAGGCACCAAGTCAGGGAAGGT 455
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DB 693 ATAGTCTTGGAGGCACCAAGTCAGGGAAGGT 725
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RESULT 15
A68828 1408 bp DNA PAT 06-MAY-1999
LOCUS Sequence 5 from Patent WO9802534.
DEFINITION A68828
ACCESSION A68828
VERSION A68828.1 GI:4759756
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1408)
AUTHORS Kieffer,B.L., Matthes,H.W., Simonin,F.H., Dierich,A. and Lemeur,M.
TITLE TRANSGENIC ANIMAL WHOSE EXPRESSION OF THE OPIATE RECEPTORS IS
MODIFIED
JOURNAL Patent: WO 9802534-A 22-JAN-1998;

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SUMMARIES

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6	20	2.0	1265	1	US-07-816-283-3
7	20	2.0	1452	1	US-08-149-093A-3
8	20	2.0	1634	2	US-08-417-103-1
9	20	2.0	1265	2	US-08-417-103-3
10	20	2.0	1205	2	US-08-417-103-13
11	20	2.0	2600	2	US-08-147-949A-1
12	20	2.0	1452	2	US-08-911-245-3
13	20	2.0	1452	2	US-08-553-058C-3
14	20	2.0	1452	3	US-08-514-451A-3
15	20	2.0	2706	3	US-08-454-549-1
16	20	2.0	1567	6	PCT-US94-10358-16
17	18	1.8	2238	1	US-07-841-651-1
18	18	1.8	1296	1	US-07-816-283-9
19	18	1.8	1296	2	US-08-417-103-9
20	18	1.8	1227	2	US-08-080-386-1
21	18	1.8	2111	4	US-08-966-316-6
22	18	1.8	1227	4	US-08-390-000A-1
23	17	1.7	489	1	US-07-879-685B-3
24	17	1.7	722	2	US-08-702-344-8
25	17	1.7	11725	3	US-08-756-506-1
26	17	1.7	1498	4	US-08-775-428-1
27	16	1.6	1351	1	US-07-816-283-5
28	16	1.6	1796	1	US-07-816-283-11
29	16	1.6	976	1	US-08-125-628-7
30	16	1.6	976	1	US-08-125-628-8
31	16	1.6	1518	1	US-08-148-215A-3
32	16	1.6	84	1	US-08-328-258-5

33	16	1.6	3505	1	US-08-454-097-34
34	16	1.6	1733	2	US-08-706-292-1
c 35	16	1.6	959	2	US-08-634-331-1
c 36	16	1.6	1899	2	US-08-634-331-2
37	16	1.6	1351	2	US-08-417-103-5
38	16	1.6	1796	2	US-08-417-103-11
39	16	1.6	1147	2	US-08-417-103-15
40	16	1.6	3505	2	US-08-468-036-43
c 41	16	1.6	2955	2	US-08-687-379-5
c 42	16	1.6	2955	2	US-08-687-379-7
43	16	1.6	6143	3	US-08-612-521-3
44	16	1.6	3505	3	US-08-376-843-43
c 45	16	1.6	959	7	5508165-1

ALIGNMENTS

RESULT 1
US-08-411-859-1
; Sequence 1, Application US/08411859
; Patent No. 5985600
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH JR., DUANE E.
; APPLICANT: EDWARDS, ROBERT H.
; TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
; TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,859
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/929,200
; FILING DATE: 13-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: LITHGOW, TIMOTHY J.
; REGISTRATION NUMBER: 36,856
; REFERENCE/DOCKET NUMBER: 22000-20526.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1829 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..1144
US-08-411-859-1

Query Match 2.9%; Score 29; DB 4; Length 1829;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 ACCATGATGAGCGTGGACCGGTACATTCG 319
|||||
Db 446 ACCATGATGAGCGTGGACCGGTACATTCG 474

RESULT 2
PCT-US94-10358-1
; Sequence 1, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
PCT-US94-10358-1

Query Match 2.6%; Score 26; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GATTACTACACATGTTCCACCAGCAT 280
|||||
Db 652 GATTACTACACATGTTCCACCAGCAT 677

RESULT 3
PCT-US94-10358-3
; Sequence 3, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas

; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 339..1235
PCT-US94-10358-3

Query Match 2.6%; Score 26; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GATTACTACACATGTTCCACCAGCAT 280
|||||
Db 652 GATTACTACACATGTTCCACCAGCAT 677

RESULT 4
PCT-US94-10358-7
; Sequence 7, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120.601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
PCT-US94-10358-7

Query Match 2.5%; Score 25; DB 6; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 TCGTCTGCTGGACTCCGATTCACAT 718
|||||
Db 1113 TCGTCTGCTGGACTCCGATTCACAT 1137

RESULT 5
US-07-816-283-1
Sequence 1, Application US/07816283
Patent No. 5436155
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-816-283-1

Query Match 2.0%; Score 20; DB 1; Length 1634;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 CAACATGTTCCACGATCT 282
|||||
Db 516 CAACATGTTCCACGATCT 535

RESULT 6
US-07-816-283-3
Sequence 3, Application US/07816283
Patent No. 5436155
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-816-283-3

Query Match 2.0%; Score 20; DB 1; Length 1265;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 CAACATGTTCCACGATCT 282
|||||
Db 504 CAACATGTTCCACGATCT 523

RESULT 7
US-08-149-093A-3
Sequence 3, Application US/08149093A
Patent No. 5658783
GENERAL INFORMATION:
APPLICANT: Bunzow, James R
APPLICANT: Grady, David K
TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific
Opioid Receptor Gene and Uses
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.125
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,093A
FILING DATE: 06-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5658783nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..181
FEATURE:
NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-08-149-093A-3

Query Match 2.0%; Score 20; DB 1; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 ACCACATTTACATATTAA 142
|||||
Db 428 ACCACATTTACATATTAA 447

RESULT 8
US-08-417-103-1
Sequence 1, Application US/08417103
Patent No. 5723299
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 100..1272
US-08-417-103-1

Query Match 2.0%; Score 20; DB 2; Length 1634;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 CAACATGTTCCACGACATCT 282
|||||
Db 516 CAACATGTTCCACGACATCT 535

RESULT 9
US-08-417-103-3
Sequence 3, Application US/08417103
Patent No. 5723299
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1260
US-08-417-103-3

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911.245
FILING DATE: 15-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149093
FILING DATE: 06-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5821067nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..181
FEATURE:
NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-08-911-245-3

Query Match 2.0%; Score 20; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ACCAACATTTACATATTAA 142
|||||
Db 428 ACCAACATTTACATATTAA 447

RESULT 13
US-08-553-058C-3
Sequence 3, Application US/08553058C
Patent No. 5821219
GENERAL INFORMATION:
APPLICANT: Grisel, Judith E.
APPLICANT: Grandy, David K.
APPLICANT: Mogil, Jeffrey S.
TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP
STREET: 121 S.W. Salmon, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: USA
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Version WP6, ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,058C
FILING DATE: 11/3/95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William D. No. 5821219nan, M.D.
REGISTRATION NUMBER: 30,878
REFERENCE/DOCKET NUMBER: 899-40006/WDN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..181
FEATURE:
NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-08-553-058C-3

Query Match 2.0%; Score 20; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ACCAACATTTACATATTAA 142
|||||
Db 428 ACCAACATTTACATATTAA 447

RESULT 14
US-08-514-451A-3
Sequence 3, Application US/08514451A
Patent No. 5837809
GENERAL INFORMATION:
APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Civeilli, Olivier
APPLICANT: Reinscheid, Rainer K.
APPLICANT: No. 5837809hacker, Hans-Peter
APPLICANT: Monsma, Frederick J.
TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston LLP
STREET: 121 S.W. Salmon, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: USA
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WP5.1 ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,451A
FILING DATE: 08/11/95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,058
FILING DATE: 11/13/95
ATTORNEY/AGENT INFORMATION:
NAME: William D. No. 5837809nan, M.D.

REGISTRATION NUMBER: 30,878
REFERENCE/DOCKET NUMBER: 899-45995/WDN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 228-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
DESCRIPTION: cdna
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..181
FEATURE:
NAME/KEY: CDS
LOCATION: 182..1282
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1283..1452
US-08-514-451A-3

Query Match 2.0%; Score 20; DB 3; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.72; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ACCAACATTTACATATTAA 142
|||||
Db 428 ACCAACATTTACATATTAA 447

RESULT 15

US-08-454-549-1
Sequence 1, Application US/08454549
Patent No. 5866324
GENERAL INFORMATION:
APPLICANT: EPPLER, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HUMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A818-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
TISSUE TYPE: Rat brain
US-08-454-549-1

Query Match 2.0%; Score 20; DB 3; Length 2706;
Best Local Similarity 100.0%; Pred. No. 0.74; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 ACCAACATTTACATATTAA 142
|||||
Db 353 ACCAACATTTACATATTAA 372

Search completed: February 17, 2000, 10:12:07
Job time: 1922 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2000, 09:50:15 ; Search time 771.69 Seconds
(without alignments)
4892.721 Million cell updates/sec

Title: US-08-455-683-11
Perfect score: 1000
Sequence: 1 AGAAGCAAAATCAGTAATC.....CCAGTAIGACTAGTCGTGGA 1000

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : BSI:*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
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31: gb_est12:*
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58: em_est26:*
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62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	78	7	8	153	22	R31984
2	33	3	3	183	22	R81583
c	20	2	0	659	63	A1980732
4	19	1	9	415	20	M75869
c	5	19	1	360	24	D75109
6	19	1	9	206	31	AA317847
7	19	1	9	521	33	AA47244

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1518 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.

FEATURES

Location/Qualifiers
1..183
/organism="Homo sapiens"
/db_xref="GB:559413"
/db_xref="taxon:9606"
/clone="IMAGE:147727"
/clone_lib="Soares placenta Nb2Hp"
/sex="female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTTCGGCGCAGGAATTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

BASE COUNT

31 a 56 c 40 g 46 t 10 others

Query Match

Best Local Similarity 3.3%; Score 33; DB 22; Length 183;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 CAACCTGGTAGGACACAGACTGGTCTGCT 676

DB 109 CAACCTGGTAGGACACAGACTGGTCTGCT 141

RESULT

AI980732/c 3
LOCUS AI980732 659 bp mRNA EST 15-SEP-1999
DEFINITION pat.pk0032.b12.f chicken activated T cell cDNA Gallus gallus cdna clone pat.pk0032.b12.f 5' similar to U1 snRNP 70K protein, mRNA sequence.

ACCESSION AI980732
VERSION AI980732.1 GI:5883760
KEYWORDS EST.

SOURCE

ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 659)
AUTHORS Tirunaguru,V.G., Sofer,L. and Burnside,J.

TITLE An expressed-sequence-tag database of activated chicken T cells: sequence analysis of 5596 clones
JOURNAL Unpublished (1995)

COMMENT On Dec 20, 1995 this sequence version replaced gi:1130941.

Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302 831-3651
Email: joan@udel.edu

Seq primer: 17.

FEATURES

Location/Qualifiers
1..659
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pat.pk0032.b12.f"
/clone_lib="chicken activated T cell cDNA"
/sex="male"
/cell_type="Con A-activated splenic T cell"

/lab_host="E.coli JOP10 F'"
/note="Vector: pCDNA3"
BASE COUNT 215 a 130 c 165 g 137 t 12 others
ORIGIN

Query Match 2.0%; Score 20; DB 63; Length 659;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 560 CCTCATCATCATCGTCTGCT 579

DB 63 CCTCATCATCATCGTCTGCT 44

RESULT

M75869 4
LOCUS M75869 415 bp mRNA EST 16-SEP-1992
DEFINITION CEL06A11 Chris Martin sorted cDNA library Caenorhabditis elegans CDNA clone cm06a11 5', mRNA sequence.

ACCESSION M75869
VERSION M75869.1 GI:275214
KEYWORDS EST.

SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.

REFERENCE 1 (bases 1 to 415)
AUTHORS Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier,L., Durbin,R.K., Green,P., Showkneen,R., Halloran,N., Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston,J.

TITLE A survey of expressed genes in Caenorhabditis elegans

JOURNAL Nature Genet. 1, 114-123 (1992)

MEDLINE 93250982

COMMENT Contact: Waterston R.H.(USA) and Sulston J.E.(UK)

(USA) Dept. of Genetics or (UK)

(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of

Molecular Biology

Box 832,4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills

Road, Cambridge CB2 2QH, UK

Tel: (USA) (314)3627072 or (UK) (0223)248011

Fax: (USA) (314)3624137 or (UK) (0223)402008

Email: rwnematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk

single read.

Location/Qualifiers

1..415

/organism="Caenorhabditis elegans"

/strain="Bristol N2"

/db_xref="taxon:6239"

/clone="cm06a11"

/lab_host="Chris Martin sorted cDNA library"

/note="Vector: lambdaDaphne SHLX2; Mixed stage

hermaphrodite cDNA library. Partially normalized by

successive picking groups of clones that didn't

hybridize to previously picked clones. Vector: lambdaDaphne

SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host:

MC1061"

BASE COUNT 123 a 69 c 95 g 125 t 3 others

ORIGIN

Query Match

Best Local Similarity 1.9%; Score 19; DB 20; Length 415;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 560 CCTCATCATCATCGTCTGCT 578

DB 78 CCTCATCATCATCGTCTGCT 96

RESULT

D75109/c
 LOCUS CELK096D7F 360 bp mRNA EST 18-OCT-1999
 DEFINITION embryo Caenorhabditis elegans CDNA clone yk96d7 5', mRNA sequence.
 JOURNAL D75109
 ACCESSION D75109.1 GI:1120893
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Kohara,Y., Mitsuiki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and Tabara,H.
 TITLE Toward an expression map of the C.elegans genome
 JOURNAL Unpublished (1994)
 COMMENT Contact: Yuji Kohara
 Gene library lab
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp
 High quality sequence stop: 322.
 FEATURES
 source
 1..360
 Location/Qualifiers
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk96d7"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaphrodite embryo"
 /sex="hermaphrodite"
 /dev_stage="embryo"
 BASE COUNT 98 a 120 c 64 g 74 t 4 others
 ORIGIN
 Query Match 1.9%; Score 19; DB 24; Length 360;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 666 CTGGTCCGTGGTGGTGG 684
 Db 173 CTGGTCCGTGGTGGTGG 155
 RESULT 6
 LOCUS AA317847 206 bp mRNA EST 19-APR-1997
 DEFINITION EST19840 Retina II Homo sapiens cDNA 5' end, mRNA sequence.
 ACCESSION AA317847
 VERSION AA317847.1 GI:1970173
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 206)
 AUTHORS Adams M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.I., Geoghagen,N.S., Glodek,A., Gnehm,C.B., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,I.A., Collins,E.J., Dinkes,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Korzak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,

Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 12140200
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1402207.
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
 FEATURES
 Location/Qualifiers
 1..206
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):118310"
 /db_xref="taxon:9606"
 /clone_lib="Retina II"
 /sex="mixed"
 /dev_stage="adult"
 /note="Organ: retina; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XbaI"
 BASE COUNT 50 a 48 c 65 g 41 t 2 others
 ORIGIN
 Query Match 1.9%; Score 19; DB 31; Length 206;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 725 CCGTGGAGGCTCTGGGG 743
 Db 48 CCGTGGAGGCTCTGGGG 66
 RESULT 7
 LOCUS AA447244 521 bp mRNA EST 03-JUN-1997
 DEFINITION ZW93C04.r1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:784518 5', mRNA sequence.
 ACCESSION AA447244
 VERSION AA447244.1 GI:2159909
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 521)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaha,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
 WashU-Merck EST Project 1997
 Unpublished (1997)
 On Apr 14, 1993 this sequence version replaced gi:692829.
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 490.
 FEATURES
 Location/Qualifiers


```

source
1. 521
/organism="Homo sapiens"
/db_xref="GDB:5982136"
/db_xref="taxon:9606"
/clone="IMAGE:784518"
/clone_lib="Soares_total_fetus_Mb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 142 a 128 c 127 g 124 t
ORIGIN

Query Match 1.9%; Score 19; DB 33; Length 521;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 725 CCTGGTGGAGCTCTGGGG 743
|||||
Db 498 CCTGGTGGAGCTCTGGGG 516

RESULT 8
AI056367
LOCUS 443 bp mRNA EST 24-SEP-1998
DEFINITION oy48c06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669066 3',
mRNA sequence.
ACCESSION AI056367
VERSION AI056367.1 GI:3330233
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/STGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1404573.
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 593 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES
source
1. 443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1669066"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"

```

```

/notes="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATATCTTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 86 a 106 c 119 g 132 t
ORIGIN

Query Match 1.9%; Score 19; DB 41; Length 443;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 435 GGCACCAAGTCAGGGAAG 453
|||||
Db 152 GGCACCAAGTCAGGGAAG 170

RESULT 9
AI524239
LOCUS 523 bp mRNA EST 18-MAR-1999
DEFINITION th11d11.x1 NCI_CGAP_CLL11 Homo sapiens cDNA clone IMAGE:2117973 3',
mRNA sequence.
ACCESSION AI524239
VERSION AI524239.1 GI:4438374
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 523)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jul 29, 1997 this sequence version replaced gi:2285735.
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco
High quality sequence stop: 434.
FEATURES
source
1. 523
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2117973"
/clone_lib="NCI_CGAP_CLL11"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATATCTTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 167 a 89 c 91 g 174 t
ORIGIN

```

Query Match 1.9%; Score 19; DB 47; Length 523;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 GGAATGCTATGTTCTT 91
 |||||
 Db 74 GGAATGCTATGTTCTT 92

RESULT 10
 AI559367 233 bp mRNA EST 12-MAY-1999
 LOCUS nt21b12.x1 NCI-CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168255 3',
 DEFINITION mRNA sequence.
 ACCESSION AI559367
 VERSION AI559367.1 GI:4509572
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 233)
 AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTGP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189024.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 568 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 224

POLYA-No. Location/Qualifiers
 1..233
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2168255"
 /clone_lib="NCI-CGAP_Brn25"
 /tissue_type="anaplastic oligodendroglioma"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGCGCATAGTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT7T3 vector.
 Library is normalized, and was constructed by Bento
 Soares and M.Fatima Bonaldo."

BASE COUNT 53 a 46 c 53 g 81 t
 ORIGIN

Query Match 1.9%; Score 19; DB 48; Length 233;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 GGCACCAAGTCAGGGAAG 453

Db 128 GGCACCAAGTCAGGGAAG 146
 |||||

RESULT 11
 AI679822/c

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 679)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Dec 20, 1995 this sequence version replaced gi:1131236.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco
 High quality sequence stop: 397.
 Location/Qualifiers
 1..679
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2255999"
 /clone_lib="NCI-CGAP_Gas4"
 /tissue_type="poorly differentiated adenocarcinoma with
 signet ring cell features"
 /lab_host="DH10B"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.69 kb. Life Technologies catalog #:
 11549-011"

BASE COUNT 102 a 207 c 207 g 163 t
 ORIGIN

Query Match 1.9%; Score 19; DB 50; Length 679;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 GAGGCACCAAGTCAGGGA 451

Db 569 GAGGCACCAAGTCAGGGA 551

RESULT 12.
 AV192296

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AV192296 378 bp mRNA EST 22-JUL-1999
 AV192296 Vujj Kohara unpublished cDNA:Strain N2 hermaphrodite
 embryo Caenorhabditis elegans cDNA clone yk603f8 5', mRNA sequence.
 ACCESSION AV192296
 VERSION AV192296.1 GI:5574448
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 378)
 Kishigaki, A., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.

TITLE

Expressed genes in C.elegans
 Unpublished (1999)
 On Jun 22, 1998 this sequence version replaced gi:3247111.

JOURNAL

Contact: Yuji Kohara

Gene Library Lab

National Institute of Genetics

Yata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.

FEATURES

Location/Qualifiers

1..378

/organism="Caenorhabditis elegans"

/strain="N2"

/db_xref="taxon:6239"

/clone="yk503f8"

/clone_lib="Yuji Kohara unpublished cDNA:Strain N2

hermaphrodite embryo"

/sex="hermaphrodite"

/dev_stage="embryo"

112 a 65 c 87 g 113 t 1 others

BASE COUNT 112 a 65 c 87 g 113 t 1 others

ORIGIN

Query Match 1.9%; Score 19; DB 62; Length 378;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 560 CCTCAICATCATCGTCTGC 578

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Db 59 CCTCAICATCATCGTCTGC 77

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source

1..523
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2471355"
 /clone_lib="NCI_CGAP Kid12"
 /tissue_type="2 pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471388-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 133 a 124 c 137 g 129 t

ORIGIN

Query Match 1.9%; Score 19; DB 63; Length 523;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GATTACTACACATGTTCA 273

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 /clone_lib="NCI_CGAP Kid12"
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 /lab_host="DH10B"
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BASE COUNT 133 a 124 c 137 g 129 t

ORIGIN

Query Match 1.9%; Score 19; DB 63; Length 523;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GATTACTACACATGTTCA 273

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1..523
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2471355"
 /clone_lib="NCI_CGAP Kid12"
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 /lab_host="DH10B"
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BASE COUNT 133 a 124 c 137 g 129 t

ORIGIN

Query Match 1.9%; Score 19; DB 63; Length 523;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GATTACTACACATGTTCA 273

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source

1..523
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2471355"
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 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471388-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 133 a 124 c 137 g 129 t

ORIGIN

Query Match 1.9%; Score 19; DB 63; Length 523;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GATTACTACACATGTTCA 273

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W P E R F E H

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Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Feb 17 11:14:53 2000; MasPar time 19.73 Seconds
Tabular output not generated.

Title: >US-08-455-683-12
Description: (1-295) from US08455683.pep
Perfect Score: 2229
Sequence: 1 YPKMKTATNIYIFNLALADA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 33.708; Variance 153.726; scale 0.219

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result		Query		Match	Length	DB	ID	Description	Pred. No.
No.	Score	%							
1	2223	99.7	295	12	R67672			Human kappa opioid re	3.49e-193
2	2192	98.3	380	27	W30297			Human kappa opioid re	2.86e-190
3	2192	98.3	380	17	R88722			Human kappa opioid re	2.86e-190
4	2192	98.3	427	27	W30298			Human kappa opioid re	2.86e-190
5	2136	95.8	380	34	W44939			Mouse kappa opiate re	5.22e-185
6	2136	95.8	380	13	R67669			Mouse kappa opioid re	5.22e-185
7	2132	95.6	380	14	R72591			Mammalian kappa opioi	1.24e-184
8	2132	95.6	380	14	R76783			Rat kappa opiate rece	1.24e-184
9	2008	90.1	424	27	W30299			Human kappa opioid re	5.44e-173
10	1524	68.4	398	34	W44937			Mouse mu opiate recep	1.16e-177
11	1522	68.3	356	11	R65188			Murine mu-subtype opi	1.78e-177
12	1522	68.3	398	14	R76781			Rat mu opiate recepto	1.78e-177
13	1522	68.3	400	13	R71966			Human mu opioid recep	2.73e-177
14	1520	68.2	398	13	R71964			Rat mu opioid recepto	2.73e-177
15	1520	68.2	400	14	R76780			Human mu opiate recep	2.73e-177
16	1452	65.1	372	14	R76782			Rat delta opiate rece	6.10e-121

SUMMARIES

17	1448	65.0	372	9	R48629			Sequence of murine de	1.44e-120
18	1448	65.0	372	13	R67670			Mouse delta opioid re	1.44e-120
19	1448	65.0	372	34	W44938			Mouse delta opiate re	1.44e-120
20	1348	60.5	371	10	R66503			Murine delta opioid r	5.80e-111
21	1345	60.3	367	13	R71968			Rat opioid receptor.	8.90e-111
22	1343	60.3	367	13	R67671			Mouse opioid receptor	8.90e-111
23	1336	59.9	367	14	R76638			Rat opiorph receptor	4.00e-110
24	1335	59.9	367	25	W26582			Rat methadone-specifi	4.95e-110
25	1335	59.9	367	36	W80549			Rat methadone-specifi	4.95e-110
26	1335	59.9	367	36	W80549			Rat methadone-specifi	4.95e-110
27	1066	47.8	367	13	R74298			Rat orphanin FQ recep	4.95e-110
28	830	37.2	391	7	R39259			Human kappa-3 opioid	2.96e-63
29	830	37.2	391	7	R39260			Murine somatostatin r	2.96e-63
30	785	35.2	369	7	R39262			Murine somatostatin r	4.01e-59
31	780	35.0	369	7	R39261			Human somatostatin re	1.15e-58
32	780	35.0	369	19	R72699			Human somatostatin re	1.15e-58
33	767	34.4	369	5	R27504			Pituitary somatostati	1.79e-57
34	736	33.0	333	13	R72985			Epsilon opioid recept	1.24e-54
35	727	32.6	322	16	R48754			Rat RGH G-protein cou	8.22e-54
36	727	32.6	322	19	W02726			Rat RGH G-protein cou	8.22e-54
37	683	30.6	418	7	R39263			Human somatostatin re	8.57e-50
38	661	29.7	428	13	R72984			Epsilon opioid recept	8.66e-48
39	658	29.5	242	23	W10017			G-protein coupled rec	1.62e-47
40	599	26.9	428	7	R39264			Murine somatostatin r	3.72e-42
41	586	26.3	241	23	W10016			G-protein coupled rec	5.60e-41
42	545	24.5	349	18	R95070			Human galanin recepto	2.84e-37
43	545	24.5	349	14	R79443			Galanin receptor.	2.84e-37
44	522	23.4	372	25	W4561			Rat galanin receptor	3.35e-35
45	522	23.4	372	29	W40135			Rat Gair2 receptor pr	3.35e-35

ALIGNMENTS

RESULT 1
ID R67672 standard; Protein; 295 AA.

AC R67672;
DE 18-AUG-1995 (first entry)
DE Human kappa opioid receptor partial protein.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 169
FT Misc_difference 181 /label= Any amino acid
FT Misc_difference 265 /label= Any amino acid
FT Misc_difference 269 /label= Any amino acid
FT Misc_difference 269 /label= Any amino acid
FT W09428132-A.
PD 08-DEC-1994.
PR 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PR (ARCH-) ARCH DEV CORP.
PR Bell GI, Reisine T, Yasuda K;
PR N-PSDB; 075931.
PR Polynucleotides and peptides derived from opioid receptor
PI screening assays for use in therapeutic compositions and in
PS Claim 12; Page 236-239; 300pp; English.
CC The partial amino acid sequence of the novel human kappa opioid receptor.
CC The corresponding gene was isolated from a human brain hippocampus cDNA
CC library using a probe from the mouse kappa opioid receptor gene (J75926).
CC The gene is missing the N-terminal sequence. The C-terminal sequence is
CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of

CC the protein in a cell. The opioid receptors thus produced are useful for
 CC the development of novel assays designed to select or improve substances,
 CC capable of interacting with the opioid receptor proteins, for use in
 CC diagnosis, drug design and therapeutic applications.
 SQ Sequence 295 AA;

Query Match 99.7%; Score 2223; DB 12; Length 295;
 Best Local Similarity 99.7%; Pred. No. 3.49e-193;
 Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 ytkmktatniyifnlaladalvttmpfsgstvlmswpgdvclkvlsidymftsi 60
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Qy 1 YTKMKTATNIYIFNLALADALVTTMPFSGSTVLMNSWPGDVCLKVLSIDYNNFTSI 60
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Db 61 ftltmsvdryiavchpvcakldfrtpkakiiniciwlissvgsaisvlggtkvregvd 120
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Qy 61 FTLTMSVDRIYAVCHPVCKALDFRTPKAKIINICILWLSSVGSISAIVLGGTKVREDVD 120
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Db 121 vieccqlfpddyswdllfmkicvffafvpyllilivcvtlmlrlkxvrlslsrek 180
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Qy 121 VIECCQLFPDDYSWDLFMKICVFFAFVPIVLIIVCYTLMIDLKXVRLSLSGREK 180
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Db 181 xnlrtrtlrvlvvavfvvcvtpihflilvealgstshstaalssvfyfialgytssln 240
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Qy 181 XNLRTRTLRVLVVAVFVVCVTPIHFLILVEALGSTSHSTAALSSVYFIALGYTNSSLN 240
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Db 241 pilayfldenfkrcfrdfcpklmmerxstsrvtvqdpaylreidgmknkpv 295
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Qy 241 PILAYFLDENFKCRDFCFPLKMMERXSTSRVTVQDPAYLREIDGMKNKPV 295
 |||||||

RESULT 2

ID W30297 standard; Protein; 380 AA.

AC W30297;

DT 14-APR-1998 (first entry)

DE Human kappa opioid receptor.

KW Selective target cell activation; G protein-coupled receptor;

KW RASL; gene therapy; cell proliferation; kappa opioid receptor;

KW human; transgenic animal; arrhythmia; bone disease; seizure;

KW vascular contraction; disease model.

OS Homo sapiens.

PH Key Location/Qualifiers

FT 1..58

FT Domain

FT /label= N-terminus

FT /note= "extracellular"

FT 59..85

FT Domain

FT /label= TMH1

FT /note= "transmembrane"

FT 86..95

FT Domain

FT /label= I1

FT /note= "cytoplasmic"

FT 96..117

FT Domain

FT /label= TMH2

FT /note= "transmembrane"

FT 118..132

FT Domain

FT /label= E2

FT /note= "extracellular"

FT 133..154

FT Domain

FT /label= TMH3

FT /note= "transmembrane"

FT 155..173

FT Domain

FT /label= I2

FT /note= "cytoplasmic"

FT 174..196

FT Domain

FT /label= TMH4

FT /note= "transmembrane"

FT 197..222

FT Domain

FT /label= E2

FT /note= "extracellular"

FT 223..247

FT Domain

FT /label= TMH5

FT /note= "transmembrane"

FT 248..275

FT /label= I3
 FT /note= "Cytoplasmic"
 FT 276..299
 FT /label= TMH6
 FT /note= "Transmembrane"
 FT 300..311
 FT /label= E3
 FT /note= "Extracellular"
 FT 312..333
 FT /label= TMH7
 FT /note= "transmembrane"
 FT 334..380
 FT /label= C-terminus
 FT /note= "cytoplasmic"
 FT 131..210
 FT Disulfide_bond
 FT Modified_site 25
 FT /note= "potential N-glycosylation"
 FT Modified_site 39
 FT /note= "potential N-glycosylation"
 FT Modified_site 345
 FT /note= "palmitate"

PN W09735478-A1.

PD 02-OCT-1997.

PF 25-MAR-1997; U05334.

PR 26-MAR-1996; US-622348.

PA (REGC) UNIV CALIFORNIA.

PI Conklin BR;

DR WPI; 97-502739/46.

DR N-PSDB; T90998.

PT Selective activation of target cell expressing modified G protein
 PT coupled receptor - allows control of cellular proliferation,
 PT especially for amplification of transfected cells in gene therapy
 PT Example 1; Page 74-76; 117pp; English.

PS This protein comprises human kappa opioid receptor (KOR), a

CC G protein-coupled receptor implicated in neurotransmission. A

CC novel method for selectively activating a target cell (TC)

CC comprises: (i) introducing into the cell a nucleic acid sequence

CC (I) that expresses a G protein-coupled receptor (A) modified to be

CC activated superiorly by a synthetic ligand (RASL); and (ii)

CC exposing the transfected cell to small synthetic molecules (B) that

CC bind to and activate (A), inducing the G protein coupled cellular

CC response associated with receptor activation. (A) has: (a)

CC decreased binding affinity for a selected natural ligand of the

CC native receptor; (b) binding affinity for (B); and (c) is activated

CC by binding (B) sufficiently to produce the required cellular

CC response. Also new are: (1) transgenic cells including

CC heterologous (I) in the genome; (2) cellular implants comprising a

CC TC transfected with (I); (3) isolated (I); and (4) transgenic

CC non-human animals expressing (A). Activation of (A) results, in

CC vitro or in vivo, in cellular proliferation, or secretion of a

CC cellular product, particularly a heterologous therapeutic protein

CC encoded by a second inserted nucleic acid sequence. Particularly

CC it is used to expand the relatively few cells that are successfully

CC transfected during gene therapy procedures. Other responses that

CC can be regulated are cell migration and contraction, or pigment

CC production. In transgenic animals, expression or stimulation of

CC (A) is designed to develop cardiac arrhythmia, symptoms of bone

CC disease, seizures, vascular contractions, dementia, neurodegeneration

CC etc., for use as models of these diseases (claimed). The transgenic

CC animals are also used for production of improved food products

CC (e.g. increased calcium content in eggshells or altered fat/lean

CC ratios) or to control fertility or induce labour. A RASL derived

CC from KOR, designated RASL ORI (see W30299), was generated by

CC mutation of the KOR cDNA sequence (see T90998).

SQ Sequence 380 AA;

Query Match 98.3%;

Best Local Similarity 97.6%;

Pred. No. 2.86e-190;

Matches 288; Conservative 1;

Mismatches 5; Indels 1;

Gaps 1;

Db 87 ytkmktatniyifnlaladalvttmpfsgstvlmswpgdvclkvlsidymftsi 146

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Qy 1 YTKMKTATNIYIFNLALADALVTTMPFSGSTVLMNSWPGDVCLKVLSIDYNNFTSI 60


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Db 147 ftltmmsvdrviavchpvcakldfrtbpkakiiniciwllssvgsaisvlggtkvredvd 206
QY 61 FTLTMSVDRVIIVAVCHPVKALDFRTPKAKIINICIWLLSSVGSISVILGGTKVREDVD 120
Db 207 viecslqfdddydwldfmlkicvifafvlpvliivcvtlmlrlksvllsgsrek 266
QY 121 VIECLQFPDDDYDWLDFMLKICVIFAFVLPVLIIVCVITLMLRLKXVLLSGSREK 180
Db 267 nllrritrlvlvavfvvcvtpbhfllvealgstshstaalsyyfcialgtyntssln 326
QY 181 XNLRIRITRLVLVAVFVVCVTPBHFILVLEALGSTSHSTAALSSYYFCIALGYTNSLN 240
Db 327 pilvafldenkrfrdcfplkmmrqrstsrvtntvqdpaylrldidgm-nkpv 380
QY 241 PILVAFLDENKFRDCFCPLKMMRQRSTSRVNTVQDPAYLRIDGMNKPV 295

RESULT 3
AC R88722 standard; Protein; 380 AA.
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis.
OS Homo sapiens.
PN W09601898-A1.
PD 23-JAN-1996. F00912.
FF 07-JUL-1995; FR-008531.
PR 11-JUL-1994; FR-008531.
PA (UNIST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B. Simonin F;
DR WPI: 96-097628/10.
DR N-PSDB; T12350.
PT New nucleic acid encoding the human kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 7: Page 13-15; 30pp; French.
CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors. The receptor can be used for identifying e.g. agonists
CC of its activity for potential use as analgesics.
SQ Sequence 380 AA;

Query Match 98.3%; Score 2192; DB 17; Length 380;
Best Local Similarity 97.6%; Pred. No. 2,856-190;
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladaivttmpfqtgsvylmmswpgdvclckivisidynnftsi 146
QY 1 YTKMKTATNIYIFNLALADALVITTMPFQSVYLMMSWPGDVCLCKIVISIDYNNFTSI 60
Db 147 ftltmmsvdrviavchpvcakldfrtbpkakiiniciwllssvgsaisvlggtkvredvd 206
QY 61 FTLTMSVDRVIIVAVCHPVKALDFRTPKAKIINICIWLLSSVGSISVILGGTKVREDVD 120
Db 207 viecslqfdddydwldfmlkicvifafvlpvliivcvtlmlrlksvllsgsrek 266
QY 121 VIECLQFPDDDYDWLDFMLKICVIFAFVLPVLIIVCVITLMLRLKXVLLSGSREK 180
Db 267 nllrritrlvlvavfvvcvtpbhfllvealgstshstaalsyyfcialgtyntssln 326
QY 181 XNLRIRITRLVLVAVFVVCVTPBHFILVLEALGSTSHSTAALSSYYFCIALGYTNSLN 240
Db 327 pilvafldenkrfrdcfplkmmrqrstsrvtntvqdpaylrldidgm-nkpv 380
QY 241 PILVAFLDENKFRDCFCPLKMMRQRSTSRVNTVQDPAYLRIDGMNKPV 295

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RESULT 4
ID W30298 standard; Protein; 427 AA.
AC W30298;
DT 14-APR-1998 (first entry)
DE Human kappa opioid receptor fusion polypeptide.
KW Selective target cell activation; G-protein-coupled receptor;
KW RASL; gene therapy; cell proliferation; kappa opioid receptor;
KW human; transgenic animal; arrhythmia; bone disease; seizure;
KW vascular contraction; disease model.
OS Chimeric - Homo sapiens.
OS Chimeric - Synthetic.
PH Key Location/Qualifiers
FT Peptide 1..30
FT /label= Sig_Peptide
FT /note= "prolactin signal sequence"
FT Peptide 31..38
FT /label= FLAG
FT Protein 39..417
FT /label= KOR
FT /note= "human kappa opioid receptor"
FT Domain 39..95
FT /label= N-terminus
FT /note= "extracellular"
FT Domain 96..122
FT /label= TMH1
FT /note= "transmembrane"
FT Domain 123..132
FT /label= I1
FT /note= "cytoplasmic"
FT Domain 133..154
FT /label= TMH2
FT /note= "transmembrane"
FT Domain 155..169
FT /label= E2
FT /note= "extracellular"
FT Domain 170..191
FT /label= TMH3
FT /note= "transmembrane"
FT Domain 192..210
FT /label= I2
FT /note= "Cytoplasmic"
FT Domain 211..233
FT /label= TMH4
FT /note= "transmembrane"
FT Domain 234..259
FT /label= E2
FT /note= "extracellular"
FT Domain 260..284
FT /label= TMH5
FT /note= "transmembrane"
FT Domain 285..312
FT /label= I3
FT /note= "Cytoplasmic"
FT Domain 313..336
FT /label= TMH6
FT /note= "transmembrane"
FT Domain 337..348
FT /label= E3
FT /note= "Extracellular"
FT Domain 349..370
FT /label= TMH7
FT /note= "transmembrane"
FT Domain 371..417
FT /label= C-terminus
FT /note= "cytoplasmic"
FT Disulfide_bond 168..247
FT Modified_site 62
FT Modified_site 76
FT Modified_site 92
FT Modified_site 382

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FT Peptide /note= "palmitate"
FT 418..427
FT /label= HA
FN WO9735478-A1.
PD 02-OCT-1997.
PF 25-MAR-1997; U05334.
PR 26-MAR-1996; US-622348.
PA (REGC ) UNIV CALIFORNIA.
PI Conklin BR;
DR WPI; 97-502739/46.
DR N-PSDB; T90999.
PT Selective activation of target cell expressing modified G protein
PT coupled receptor - allows control of cellular proliferation,
PT especially for amplification of transfected cells in gene therapy
PS Example 1; Page 77-79; 117pp; English.
CC This polypeptide comprises the human G protein-coupled kappa
CC opiod receptor (KOR) (see also W30297) flanked by N- and
CC C-terminal sequences that facilitate the detection and
CC purification of recombinant KOR, and especially KOR RASLS (see
CC W30299), i.e. a receptor activated superiorly by a synthetic
CC ligand. A novel method for selectively activating a target cell
CC (TC) comprises: (i) introducing into the cell a nucleic acid
CC sequence (I) that expresses a RASSL (A) and (ii) exposing the
CC transfected cell to small synthetic molecules (B) that bind to and
CC activate (A), inducing the G protein coupled cellular response
CC associated with receptor activation. (A) has: (a) decreased binding
CC affinity for a selected natural ligand of the native receptor; (b)
CC binding affinity for (B); and (c) is activated by binding (B)
CC sufficiently to produce the required cellular response. Also new
CC are: transgenic cells including heterologous (I) in the genome;
CC cellular implants comprising a TC transfected with (I); isolated
CC (I); and transgenic animals expressing (A). Activation of (A)
CC results, in vitro or in vivo, in cellular proliferation, or
CC secretion of a cellular product, particularly a heterologous
CC therapeutic protein encoded by a second inserted nucleic acid
CC sequence. Particularly it is used to expand the relatively few
CC cells that are successfully transfected during gene therapy
CC procedures. Other responses that can be regulated are cell
CC migration and contraction, or pigment production. In transgenic
CC animals, expression or stimulation of (A) is designed to develop
CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC contractions, dementia, neurodegeneration etc., for use as models
CC of these diseases (claimed). The transgenic animals are also used
CC for production of improved food products (e.g. increased calcium
CC content in eggshells or altered fat/lean ratios) or to control
CC fertility or induce labour.
SQ Sequence 427 AA;

Query Match 98.3%; Score 2192; DB 27; Length 427;
Best Local Similarity 97.6%; Pred. No. 2,86e-190;
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 124 ytkmktatniyifnlaladalvtttmpfgstvyilmnspfgdvlckivisidyygmfts 183
QY 1 YTKMKTATNIYIFNLALADALVTTTMPFQSTVYILMNSWPFGLVCKIVISIDYNNMFTSI 60

Db 184 fultmmsvdyriavchpvcaldfrtptlkakiniicwllssvgsaisavlsgtkvredvd 243
QY 61 FULTMMSVDRIYAVCHPVKALDFRTPLKAKIINICWLLSSVGSISAVLGGTKVREDVD 120

Db 244 vlecslqfddyswddlfmkicvtfafvfpvliiivcylmrlkksvllsgsrek 303
QY 121 VIECCLOPDDDDYSWDDLFMKICVFIFAFVPLVLIIVCYILMILRLKXVRLSSGREK 180

Db 304 nrlrritrlvlvvaavfvcwtpthifilvealgstshstaalssyfficialgynssln 363
QY 181 NXLRRITRLVLVVAVFVVCWTPTHIFILVEALGSTSHSTAALSSYFFICIALGYNSSLN 240

Db 364 pilyafldenfkrcfrcfcpkmmqrqstsrvtntvqdpaylrdidgm-nkpv 417
QY 241 PILYAFLDENFKRCRDFCFPLKMMXERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 5
ID W44939 standard; Protein; 380 AA.
AC W44939;
DE 28-OCT-1998 (first entry)
DE Mouse kappa opiate receptor.
KW Mouse; kappa opiate receptor; transgenic animal; mammal; identification;
KW exon; nervous tissue; pain; drug addiction; transplant rejection;
KW immunosuppressant; analgesic; morphine; side effect.
OS Mus sp.
PN WO9802534-A2.
PD 22-JAN-1998.
PE 11-JUL-1997; F01282.
PR 15-JUL-1996; FR-008610.
PA (CNRS ) CENT NAT RECH SCI.
PI Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;
DR WPI; 98-110582/10.
DR N-PSDB; V49254.
PT Transgenic animals defective in one type of opiod receptor - used
PT to identify agents for treatment of pain, drug addiction and
PT transplant rejection, lacking side effects of known opiate(s)
PS Disclosure; Fig 13; 58pp; French.
CC This sequence represents the mouse kappa opiate receptor. The gene
CC sequence is used to generate a transgenic non-human mammal for
CC identifying agents for treating disorders associated with opiate
CC receptors. In the mammal, the expression of the gene encoding the
CC opiate receptor is modified, particularly by the deletion of an exon
CC and/or insertion of a marker gene, e.g. the neomycin resistance gene,
CC into the sequence. Especially the expression of the gene is altered
CC in nervous tissue. The agents are potentially useful for treating or
CC severe pain (chronic or acute), drug addiction and/or prevention or
CC treatment of transplant rejection (as immunosuppressants). The method
CC may isolate and identify powerful analgesics that lack morphine-like
CC side effects.
SQ Sequence 380 AA;

Query Match 95.8%; Score 2136; DB 34; Length 380;
Best Local Similarity 92.9%; Pred. No. 5,22e-185;
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtttmpfgsavilmnspfgdvlckivisidyygmfts 145
QY 1 YTKMKTATNIYIFNLALADALVTTTMPFQSTVYILMNSWPFGLVCKIVISIDYNNMFTSI 60

Db 147 fultmmsvdyriavchpvcaldfrtptlkakiniicwllssvgsaisavlsgtkvredvd 206
QY 61 FULTMMSVDRIYAVCHPVKALDFRTPLKAKIINICWLLSSVGSISAVLGGTKVREDVD 120

Db 207 vlecslqfddyswddlfmkicvtfafvfpvliiivcylmrlkksvllsgsrek 266
QY 121 VIECCLOPDDDDYSWDDLFMKICVFIFAFVPLVLIIVCYILMILRLKXVRLSSGREK 180

Db 267 nrlrritrlvlvvaavfvcwtpthifilvealgstshstaalssyfficialgynssln 326
QY 181 NXLRRITRLVLVVAVFVVCWTPTHIFILVEALGSTSHSTAALSSYFFICIALGYNSSLN 240

Db 327 pilyafldenfkrcfrcfcpkmmqrqstsrvtntvqdpasmrdvsgm-nkpv 380
QY 241 PILYAFLDENFKRCRDFCFPLKMMXERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 6
ID R67669 standard; Protein; 380 AA.
AC R67669;
DE 17-AUG-1995 (first entry)
DE Mouse kappa opiod receptor MORK1.
KW Mouse; kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeic; assay; probe.
OS Mus musculus.
PN WO9428132-A.
PD 08-DEC-1994.
PE 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.

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30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PR (ARCH-) ARCH DEV CORP.
PA Bell GI, Reisine I, Yasuda K;
DR WPI: 95-022804/03.
DR N-PSDB; Q75926.
DR Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 8: Page 207-211; 300pp; English.
CC The amino acid sequence of the novel mouse kappa opioid receptor mORK1.
CC The corresponding gene was isolated from a mouse brain cDNA library using
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRIF) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb pST1 fragment from the mouse
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV
CC promoter-based expression vector pCMV-6b. The resultant construct
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
CC Sequence 380 AA;
SQ

Query Match 95.8%; Score 2136; DB 13; Length 380;
Best Local Similarity 92.9%; Pred. No. 5.22e-185;
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 87 ytkmktatniyfnladalalvtttmpqfsgavylmmswpgfdvckivisidyvnmftsi 146
QY 1 YTKMKTATNIYFNALADALVTTTTPFQSTVYLMNSWPGFDVCKIVISIDYVNMFTSI 60

Db 147 flltmsvdryiavchpwkaldfrtpkakiiniwiilassvsaivlggtkvredvd 206
QY 61 FLLTMSVDRYIAVCHPWKALDFRTPKAKIINICWILSSVGSIAVLGGTKVREDVD 120

Db 207 vicslqfpdedswwdlfmkicvtfafvipvlilivcvtlmlirksvrlslgsrskd 266
QY 121 VIECCLQFPDDDSWDLFMKICVTFAFVIPVLIIIVCYILMLIRLAKXVLLSGSRKED 180

Db 267 nrlritklvllvvavvfiicwtpihifilvealgstshstaalsyycialgvtssln 326
QY 181 XNLRIRIRLVLVVAVVVCWPIPIHIFILVEALGSTSHSTAALSSYFCIALGVTSSLN 240

Db 327 pvlvafldenfricrfdcfpikmmerqstsrvtntvgdpasrmdvqgm-nkpyv 380
QY 241 PVLVAFLDENFRCRFDCCFPIKMXERXSTRVNTVQDPAYLRIDGMKNKPY 295

RESULT 7
ID R72591 standard; Protein: 380 AA.
AC R72591;
DT 01-DEC-1995 (first entry)
DE Mammalian kappa opioid receptor protein.
KW Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
CS Rattus rattus.
FH Key Location/Qualifiers
FT cds 111..1253
FT /*tag= a
FT /*product= kappa opioid receptor
FN J07070191-A.
PD 14-MAR-1995.
PF 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PA (TAKE) TAKEDA CHEM IND LTD.
DR WPI: 95-144857/19.
DR N-PSDB; Q86725.
PT kappa opioid receptor protein and cells expressing it - useful
PT for the screening of compounds for analgesic and hypnotic

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PT properties
PS Claim 2; Page 9-10; 15pp; Japanese.
CC The amino acid sequence of the novel mammalian kappa opioid receptor.
CC The gene was isolated by amplifying a fragment from rat brain mRNA by
CC reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC the mouse delta-opioid receptor gene. This fragment was cloned into the
CC plasmid pCRII to produce pRII. The plasmid pRII was used to probe a rat
CC brain DNA library in lambda ZAP1 to obtain a clone of the rat kappa
CC opioid receptor gene, designated pkOR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SQ Sequence 380 AA;

Query Match 95.6%; Score 2132; DB 14; Length 380;
Best Local Similarity 92.5%; Pred. No. 1.24e-184;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtttmpfsgsavlmswfgdvclkvivisidyyymftsI 146
QY 1 YTRKMTATNIYIFNLALADALVTITMPFSGSYVLMNSWFGDVCLKVIVISIDYYNMFTSI 50
Db 147 ftltmmsvdrivavchbpvkaldfrtltkakiniciwllassvgisavlqgtkvredvd 206
QY 61 FTLTMSVDRIIVACHBPVKALDRTPLKAKIINICWLLSSVGSISAVLIGTKRVREDVD 120
Db 207 viecsiqfbddeyswwdlfmkicvfafvipvliiivcvtimilrksvriilsgsrekd 266
QY 121 VIECQLQFPDDYSWDLFMKICVFVAFVIPVLIIVCIVTLMILRLKXVRLSSGSRKED 180
Db 267 rnlrrtklrvvavfiicwtppihifilvealgstshstavlssyvfciatgynssln 326
QY 181 XNLRRITRLVWVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYVFICATLGYNSSLN 240
Db 327 pvlvafidenkfcfrdfcfdpikmmrgstarrvntdgpasmrdvggm-ekpv 380
QY 241 PVLVAFIDENKFCFRDFCFDPIKMMRGSTARRVNTDGPASMRDVGGM-EKPV 295

RESULT 8
ID R76783 standard; Protein; 380 AA.
AC R76783;
DT 11-DEC-1995 (first entry)
DE Rat kappa opiate receptor.
KW kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;
KW opiate antagonist; drug abuse; analgesic.
OS Rattus sp.
PN W09520667-A1.
PD 30-AUG-1995.
PF 30-JAN-1994; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
PR WP; 95-275452/36.
DT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PS Disclosure: Page 29-30; 49pp; English.
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R76781-83).
SQ Sequence 380 AA;

Query Match 95.6%; Score 2132; DB 14; Length 380;
Best Local Similarity 92.5%; Pred. No. 1.24e-184;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 ytkmktatniyifnlaladalvtttmpfsgsavlmswfgdvclkvivisidyyymftsI 146
QY 1 YTRKMTATNIYIFNLALADALVTITMPFSGSYVLMNSWFGDVCLKVIVISIDYYNMFTSI 50
Db 147 ftltmmsvdrivavchbpvkaldfrtltkakiniciwllassvgisavlqgtkvredvd 206

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QY 61 FFLTMSVDRYTAVCPKALDFRPLKAKIINICWLLSSVGSIAVLGCTKREDYD 120
D 207 vieclqfpddeswdfmkvcvfvafvlpvllivcytllmrlkvsrllsgsrek 266
QY 121 VTECCLQFPDDYSWDFMKTCVIFAFVIFVPLIIVCYTIMLRLKXVRLSGSREK 180
D 267 nrlritklvlvavfciwtpihflilvealgtstshstavlssyfyfciaglyntssin 326
QY 181 XNLRITRLVAVVAVFVVCWPIHIFILVEALGTSTSHSTAAALSSYFVFCIALGYNTSSLN 240
D 327 pylvlfdenfkrfirdfcpikmmergstarrvntvdpsmrdvqgm-nkpv 380
QY 241 PILIYAFLDENFRCFRDFCFPLKXMXERXSTSRVNTVDQPAYLREIDGMNKP 295

RESULT 9
ID W30299 standard; Protein; 424 AA.
AC W30299;
DT 14-APR-1998 (first entry)
DE Human kappa opioid receptor RASSL ORL.
KW Selective target cell activation; G protein-coupled receptor;
KW RASSL; gene therapy; cell proliferation; kappa opioid receptor;
KW human; transgenic animal; arrhythmia; bone disease; seizure;
KW vascular contraction; disease model.
OS Chimeric - Homo sapiens.
OS Chimeric - Synthetic.
FH key Location/Qualifiers
FT Peptide 1..30
FT /label= Sig peptide
FT /note= "prolactin signal sequence"
FT Peptide 31..38
FT /label= FLAG
FT Protein 39..414
FT /label= KOR
FT /note= "human kappa opioid receptor"
FT Domain 39..95
FT /label= N-terminus
FT /note= "extracellular"
FT Domain 96..122
FT /label= TMH1
FT /note= "transmembrane"
FT Domain 123..132
FT /label= I1
FT /note= "cytoplasmic"
FT Domain 133..154
FT /label= TMH2
FT /note= "transmembrane"
FT Domain 155..169
FT /label= E2
FT /note= "Extracellular"
FT Domain 170..191
FT /label= TMH3
FT /note= "transmembrane"
FT Domain 192..210
FT /label= I2
FT /note= "Cytoplasmic"
FT Domain 211..233
FT /label= TMH4
FT /note= "transmembrane"
FT Domain 234..259
FT /label= E2
FT /note= "extracellular, contains 17 amino acid
FT residues from delta opioid receptor
FT (Val-235, Gln-237, Pro-238, Asp-240,
FT Gly-241, Ala-242, Val-243, Val-244,
FT Thr-246, Ser-251, Pro-252, Ser-253,
FT Trp-254, Tyr-255, Thr-258, Val-259,
FT Thr-260)"
FT Domain 260..281
FT /label= TMH5
FT /note= "transmembrane"
FT Domain 282..309

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FT /label= I3
FT /note= "Cytoplasmic"
FT Domain 310..333
FT /label= TMH6
FT /note= "Transmembrane"
FT Domain 334..345
FT /label= E3
FT /note= "Extracellular"
FT Domain 346..367
FT /label= TMH7
FT /note= "transmembrane"
FT Domain 368..414
FT /label= C-terminus
FT /note= "cytoplasmic"
FT Disulfide_bond 168..245
FT Modified_site 62
FT /note= "potential N-glycosylation"
FT Modified_site 76
FT /note= "potential N-glycosylation"
FT Modified_site 382
FT /note= "palmitate"
FT Peptide 415..424
FT /label= HA
PN W09735478-A1.
PD 02-OCT-1997.
PF 25-MAR-1997; U05334.
PR 26-MAR-1996; US-622348.
PA (REGC ) UNIV CALIFORNIA.
PI Conklin BR.
DR WPI: 97-502739/45.
DR N-PSDB; T92601.
PT Selective activation of target cell expressing modified G protein
PT coupled receptor - allows control of cellular proliferation,
PT especially for amplification of transfected cells in gene therapy
PS Example 1: Page 80-82; 117pp; English.
CC This protein comprises RASSL ORL, a G protein-coupled receptor that
CC is activated superiorly by synthetic ligands. ORL comprises human
CC G protein-coupled kappa opioid receptor (KOR) (see also W30297)
CC modified at 17 amino acid positions to contain the corresponding
CC amino acid of the delta opioid receptor, and containing N- and
CC C-terminal flanking sequences that facilitate the detection and
CC purification of recombinant protein. A novel method for selectively
CC activating a target cell (TC) comprises: (A) introducing into the
CC cell a nucleic acid sequence (I) (see T92601) that expresses a RASSL
CC (A) and (ii) exposing the transfected cell to small synthetic molecules
CC (B) that bind to and activate (A), inducing the G protein coupled
CC cellular response associated with receptor activation. (A) has: (a)
CC decreased binding affinity for a selected natural ligand of the
CC native receptor; (b) binding affinity for (B); and (C) is activated
CC by binding (B) sufficiently to produce the required cellular response.
CC Also new are: transgenic cells including heterologous (I) in the
CC genome; cellular implants comprising a TC transfected with (I);
CC isolated (I); and transgenic animals expressing (A). Activation of
CC (A) results, in vitro or in vivo, in cellular proliferation, or
CC secretion of a cellular product, particularly a heterologous
CC therapeutic protein encoded by a second inserted nucleic acid
CC sequence. Particularly it is used to expand the relatively few
CC cells that are successfully transfected during gene therapy
CC procedures. Other responses that can be regulated are cell
CC migration and contraction, or pigment production. In transgenic
CC animals, expression or stimulation of (A) is designed to develop
CC cardiac arrhythmia, symptoms of bone disease, seizures, vascular
CC contractions, dementia, neurodegeneration etc., for use as models
CC of these diseases (claimed). The transgenic animals are also used
CC for production of improved food products (e.g. increased calcium
CC content in eggshells or altered fat/lean ratios) or to control
CC fertility or induce labour.
SQ Sequence 424 AA;

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Query Match 90.1%; Score 2008; DB 27; Length 424;
 Best Local Similarity 91.2%; Pred. No. 5.44e-173;
 Matches 269; Conservative 4; Mismatches 18; Indels 4; Gaps 4;

Db 124 ytkmktatniyifnlaladalattttmpfgstvlmswpgdvclkvlsidvymftsi 183
 QY 1 YTKMKTATNIYIFNLALADALVTTMPFGSTVYLMNSWPGDVCLKVLSIDYNNFTSI 60
 Db 184 fltmsvdrylavchpvcakldfrtplkakiniicllwlassvgisaivlgtqrdga- 242
 QY 61 FLTMSVDRYIAVCHPVKALDFTPLKAKIINIICLLWSSVGSIAIVLGTQKVEDVD 120
 Db 243 vv-ctlgfsspw-yvdtvttkicvffafvlpvliivcytlmiilrksvrlsgrskd 300
 QY 121 VIECCLOFPDDDDYSWDLFMKICVFFAFVLPVLIIVCYTLMILRLKXVRLSSGREK 180
 Db 301 rnlrritrlvllvvavfvvcwtpihifilvealgstshstaalssyfficalgytnssln 360
 QY 181 XNLRITRLVLLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFFICALGYTNSSLN 240
 Db 361 pilyafldenkrfcrdfcplkmrgerstsvrntvdpaylridgm-nkpv 414
 QY 241 PILYAFLDENKRCRDFCPLKMXMERXSTSVRNTVQDPAYLREIDGMNKPV 295

RESULT 10

ID W4937 standard; Protein; 398 AA.
 AC W4937;
 DT 28-OCT-1998 (first entry)
 DE Mouse mu opiate receptor.
 KW Mouse; mu opiate receptor; transgenic animal; mammal; identification;
 KW exon; nervous tissue; pain; drug addiction; transplant rejection;
 KW immunosuppressant; analgesic; morphine; side effect.
 OS Mus sp.
 PN W09802534-A2.
 PD 22-JAN-1998.
 PF 11-JUL-1997; F01282.
 PR 15-JUL-1996; PR-008810.
 PA (CNRS) CENT NAT RECH SCI.
 PI Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;
 DR WPI: 98-110582/10.
 DR N-PSDB; V49252.
 PT Transgenic animals defective in one type of opiate receptor - used
 PT to identify agents for treatment of pain, drug addiction and
 PT transplant rejection, lacking side effects of known opiate(s)
 PS Disclosure; Fig 11; 58pp; French.
 CC This sequence represents the mouse mu opiate receptor. The gene sequence
 CC is used to generate a transgenic non-human mammal for identifying agents
 CC for treating disorders associated with opiate receptors. In the mammal,
 CC the expression of the gene encoding the opiate receptor is modified,
 CC particularly by the deletion of an exon and/or insertion of a marker
 CC gene, e.g. the neomycin resistance gene, into the sequence. Especially
 CC the expression of the gene is altered in nervous tissue. The agents are
 CC potentially useful for treating severe pain (chronic or acute), drug
 CC addiction and/or prevention or treatment of transplant rejection (as
 CC immunosuppressants). The method may isolate and identify powerful
 CC analgesics that lack morphine-like side effects.
 SQ Sequence 398 AA;

Query Match 68.4%; Score 1524; DB 34; Length 398;
 Best Local Similarity 65.7%; Pred. No. 1.16e-127;
 Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;

Db 96 ytkmktatniyifnlaladalattttmpfgsvlmgtwfgtlckivlsidvymftsi 155
 QY 1 YTKMKTATNIYIFNLALADALVTTMPFGSTVYLMNSWPGDVCLKVLSIDYNNFTSI 60
 Db 156 fltctmsvdrylavchpvcakldfrtprnakivncvllsssaiglpvmfmatkvrqg-s 214
 QY 61 FLTMSVDRYIAVCHPVKALDFTPLKAKIINIICLLWSSVGSIAIVLGTQKVEDVD 120
 Db 215 -ldctltfshptw-ywenllkicvffafimpvliitvcygmilrlksvrlsgrskd 272
 QY 121 VIECCLOFPDDDDYSWDLFMKICVFFAFVLPVLIIVCYTLMILRLKXVRLSSGREK 180
 Db 273 rnlrritrlvllvvavfvvcwtpihifilvealgstshstaalssyfficalgytnscin 332
 QY 181 XNLRITRLVLLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFFICALGYTNSSLN 240

QY 181 XNLRITRLVLLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFFICALGYTNSSLN 240
 Db 333 pilyafldenkrfcrdfcplkmrgerstsvrntvdpaylridgm-nkpv 414
 QY 241 PILYAFLDENKRCRDFCPLKMXMERXSTSVRNTVQDPAYLREID 288

RESULT 11

ID R65188 standard; Protein; 356 AA.
 AC R65188;
 DT 19-APR-1995 (first entry)
 DE Murine mu-subtype opiate receptor.
 KW Mu-subtype opiate receptor; MSOR; drug addiction.
 OS Rattus rattus.
 FH Key Location/Qualifiers
 FT modified_site 10..12
 FT modified_site 230
 FT /note= "Putative N-linked glycosylation site"
 FT /note= "Threonine residue especially favourable
 FT for protein kinase A phosphorylation"
 FT region 25..48
 FT /note= "hydrophobic membrane spanning region"
 FT region 58..78
 FT /note= "hydrophobic membrane spanning region"
 FT region 96..118
 FT /note= "hydrophobic membrane spanning region"
 FT region 139..166
 FT /note= "hydrophobic membrane spanning region"
 FT region 187..212
 FT /note= "hydrophobic membrane spanning region"
 FT region 236..257
 FT /note= "hydrophobic membrane spanning region"
 FT region 274..294
 FT /note= "hydrophobic membrane spanning region"

PN EP-612845-A.
 PD 31-AUG-1994.
 PF 09-FEB-1994; 101968.
 PR 26-FEB-1993; US-026140.
 PA (AMCY) AMERICAN CYANAMID CO.
 PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;
 DR WPI; 94-265963/33.
 DR N-PSDB; Q79199.
 PT Pure mu-type opiate receptor protein - and nucleic acid coding
 PT for it
 PS Claim 2; fig 9; 39pp; English.
 CC R65188 is the rat mu-subtype opiate receptor protein purified
 CC from rat brain membranes, with biotinyl-B-endorphin (R56666)
 CC as its ligand. It is encoded by the nucleotide sequence Q79199
 CC which was synthesised using Q71022 and Q71023 as PCR primers.
 CC R65188 is useful for identifying other receptor subtypes, for
 CC screening new opiate ligands, and for studying mechanisms of
 CC opiate action, e.g. drug addiction.
 SQ Sequence 356 AA;

Query Match 68.3%; Score 1522; DB 11; Length 356;
 Best Local Similarity 66.1%; Pred. No. 1.78e-127;
 Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;

Db 54 ytkmktatniyifnlaladalattttmpfgsvlmgtwfgtlckivlsidvymftsi 113
 QY 1 YTKMKTATNIYIFNLALADALVTTMPFGSTVYLMNSWPGDVCLKVLSIDYNNFTSI 60
 Db 114 fltctmsvdrylavchpvcakldfrtprnakivncvllsssaiglpvmfmatkvrqg-s 172
 QY 61 FLTMSVDRYIAVCHPVKALDFTPLKAKIINIICLLWSSVGSIAIVLGTQKVEDVD 120
 Db 173 -ldctltfshptw-ywenllkicvffafimpvliitvcygmilrlksvrlsgrskd 230
 QY 121 VIECCLOFPDDDDYSWDLFMKICVFFAFVLPVLIIVCYTLMILRLKXVRLSSGREK 180
 Db 231 rnlrritrlvllvvavfvvcwtpihifilvealgstshstaalssyfficalgytnscin 290
 QY 181 XNLRITRLVLLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFFICALGYTNSSLN 240

Db 291 pviyafldenfkrcfrcfstieqgnstrvgrntrehpstantvd 339
 QY 241 PILYAFDENKRCFRDCEFLKMXMERXSTSRV-NTVQDPAYLREID 288

RESULT 12
 ID R76781 standard; Protein; 398 AA.

AC R76781;
 DT 11-DEC-1995 (first entry)
 DE Rat mu opiate receptor.
 KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
 OS drug abuse; analgesic.
 PN WO9520667-A1.
 PD 03-AUG-1995.
 PF 30-JAN-1995; U01144.
 PR 28-JAN-1994; US-188275.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI (USSH) US SEC DEPT HEALTH.
 FI Johnson PS, Persico AM, Uhl G, Wang J;
 DR WPI; 95-275452/36.
 PT New DNA encoding human mu opiate receptor - used esp. for screening
 PT cpts. for activity as opiate agonists or antagonists
 PS Disclosure; Page 26-28; 49pp; English.
 CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. The encoded
 CC protein showed homology to rat mu, delta and kappa opiate
 CC receptors (R76781-83).
 SQ Sequence 398 AA;

Query Match 68.3%; Score 1522; DB 14; Length 398;
 Best Local Similarity 66.1%; Pred. No. 1.78e-127;
 Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;

Db 96 ytkmktatniyifnladalatatstlqfsgvnylmtwfgtllckivisidynnftsi 155
 QY 1 YTKMKTATNIYIFNLADALVTTTFPGSTVYLMNSWPGDVLCKIVISIDYNNFTSI 60
 Db 156 ftlctmsvdrviavchpvcakldfrtprnakivncwllssaisgipvmfmatkrygg-s 214
 QY 61 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICILWLLSSVGSIAIVLGGTKVREDVD 120
 Db 215 -idctltfshtw-ywenllkicvfafimpvliitvcyglmilrlksvrmisgsked 272
 QY 121 VIECCIQFPDDDDYSWDLFMKICVFIFAFVPIVLLIIVCYTLMILRLKXVRLLSGSKED 180
 Db 273 rnlrritrmvlvavfvcwtpihyviakalitipettfqvswfhcicalgytncsln 332
 QY 181 XNLRIRLRLVIVVAVFVVCWTFIHFILVEALGSGTSHSTAALSSYFYFCIALGYTNSLN 240
 Db 333 pviyafldenfkrcfrcfstieqgnstrvgrntrehpstantvd 381
 QY 241 PILYAFDENKRCFRDCEFLKMXMERXSTSRV-NTVQDPAYLREID 288

RESULT 13
 ID R71966 standard; Protein; 400 AA.

AC R71966;
 DT 20-OCT-1995 (first entry)
 DE Human mu opiate receptor.
 KW Mu opiate receptor; MOR; gene therapy; diagnostic.
 OS Homo sapiens.
 PN WO9507983-A.
 PD 23-MAR-1995.
 PF 13-SEP-1994; U10358.
 PR 13-SEP-1993; US-120601.
 PA (INDV) UNIV INDIANA FOUND.
 PI Yu L;
 DR WPI; 95-131351/17.
 DR N-PSDB; Q89226.
 PT New nucleic acid encoding new human mu opiate receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in

PT diagnosis, treatment and drug screening.
 PS Claim 4; Page 211-214; 266pp; English.
 CC A cDNA library constructed from human caudate nucleus mRNA was
 CC screened with rat mu opiate receptor cDNA under conditions of
 CC low stringency. One positive clone included the sequence given in
 CC Q89226, encoding a mu opiate receptor MOR (R71964). The cDNA
 CC is used for prodn. of recombinant MOR, in gene therapy, etc.
 SQ Sequence 400 AA;

Query Match 68.3%; Score 1522; DB 13; Length 400;
 Best Local Similarity 67.1%; Pred. No. 1.78e-127;
 Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db 98 ytkmktatniyifnladalatatstlqfsgvnylmtwfgtllckivisidynnftsi 157
 QY 1 YTKMKTATNIYIFNLADALVTTTFPGSTVYLMNSWPGDVLCKIVISIDYNNFTSI 60
 Db 158 ftlctmsvdrviavchpvcakldfrtprnakivncwllssaisgipvmfmatkrygg-s 216
 QY 61 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICILWLLSSVGSIAIVLGGTKVREDVD 120
 Db 217 -idctltfshtw-ywenllkicvfafimpvliitvcyglmilrlksvrmisgsked 274
 QY 121 VIECCIQFPDDDDYSWDLFMKICVFIFAFVPIVLLIIVCYTLMILRLKXVRLLSGSKED 180
 Db 275 rnlrritrmvlvavfvcwtpihyviakalitipettfqvswfhcicalgytncsln 334
 QY 181 XNLRIRLRLVIVVAVFVVCWTFIHFILVEALGSGTSHSTAALSSYFYFCIALGYTNSLN 240
 Db 335 pviyafldenfkrcfrcfstieqgnstrvgrntrehpstantvd 374
 QY 241 PILYAFDENKRCFRDCEFLKMXMERXSTSRVNTVQD 280

RESULT 14
 ID R71964 standard; Protein; 398 AA.

AC R71964;
 DT 20-OCT-1995 (first entry)
 DE Rat mu opiate receptor.
 KW Mu opiate receptor; MOR-1; gene therapy; diagnostic.
 OS Rattus sp.
 PN WO9507983-A.
 PD 23-MAR-1995.
 PF 13-SEP-1994; U10358.
 PR 13-SEP-1993; US-120601.
 PA (INDV) UNIV INDIANA FOUND.
 PI Yu L;
 DR WPI; 95-131351/17.
 DR N-PSDB; Q89222.
 PT New nucleic acid encoding new human mu opiate receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 PS Disclosure; Page 190-194; 266pp; English.
 CC A 365 bp fragment of the mouse delta opiate receptor was used to
 CC screen a rat brain cDNA library under low stringency conditions.
 CC One positive clone included the sequence given in Q89222, encoding a
 CC mu opiate receptor, MOR-1 (R71964). MOR-1 was stably expressed in
 CC transfected CHO cells.
 SQ Sequence 398 AA;

Query Match 68.2%; Score 1520; DB 13; Length 398;
 Best Local Similarity 65.7%; Pred. No. 2.73e-127;
 Matches 190; Conservative 46; Mismatches 49; Indels 4; Gaps 4;

Db 96 ytkmktatniyifnladalatatstlqfsgvnylmtwfgtllckivisidynnftsi 155
 QY 1 YTKMKTATNIYIFNLADALVTTTFPGSTVYLMNSWPGDVLCKIVISIDYNNFTSI 60
 Db 156 ftlctmsvdrviavchpvcakldfrtprnakivncwllssaisgipvmfmatkrygg-s 214
 QY 61 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICILWLLSSVGSIAIVLGGTKVREDVD 120
 Db 215 -idctltfshtw-ywenllkicvfafimpvliitvcyglmilrlksvrmisgsked 272

QY	121	VIECCLOFPDDYSSWDLFMKICVFIFAFVPIVLIIVCYITIMELFKKXVRLISGREKD	180
Db	273	rnlrtrrmvlvvavfvcwtbpihiyvaikalitipettqvtswfhcfaigytnascln	332
QY	181	XNLRRITRLVLVVAVFVVCWTPIHIFILVEALGSHSTALSSYFFCIALCYINSSLN	240
Db	333	pvlvafldenkfrcfrefcldptstieqcnqstrvrgntrehpstantvd	381
QY	241	PIIYAFLDENKFCRDFCPFLKMMXERXSTSRVR-NIVQDPAYLEID	288
RESULT 15			
ID	R76780	standard; Protein; 400 AA.	
AC	R76780;		
DT	11-DEC-1995	(first entry)	
DE	Human mu opiate receptor.		
KW	Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;		
KW	drug abuse; analgesic.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	modified_site	9	
FT		/label= Glycosylation	
FT		/note= 'N-linked glycosylation site'	
FT	modified_site	11	
FT		/label= Glycosylation	
FT		/note= 'N-linked glycosylation site'	
FT	modified_site	32	
FT		/label= Glycosylation	
FT		/note= 'N-linked glycosylation site'	
FT	modified_site	40	
FT		/label= Glycosylation	
FT		/note= 'N-linked glycosylation site'	
FT	modified_site	48	
FT		/label= Glycosylation	
FT		/note= 'N-linked glycosylation'	
FT	domain	68..87	
FT		/label= Transmembrane_domain	
FT	domain	107..125	
FT		/label= Transmembrane_domain	
FT	domain	144..165	
FT		/label= Transmembrane_domain	
FT	domain	188..208	
FT		/label= Transmembrane_domain	
FT	domain	236..256	
FT		/label= Transmembrane_domain	
FT	domain	284..304	
FT		/label= Transmembrane_domain	
FT	domain	322..341	
FT		/label= Transmembrane_domain	

PI	WO9520667-A1.
PD	03-AUG-1995.
PD	30-JAN-1995. U01144.
PF	30-JAN-1994; US-188275.
PR	28-JAN-1994; US DEPT HEALTH & HUMAN SERVICES.
PPA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PPA	(USSH) US SEC DEPT HEALTH.
PI	Johnson PS, Persico AM, Uhl G, Wang J;
PI	WPI; 95-275452/36.
DR	N-PSDB: Q93102.
PI	New DNA encoding human mu opiate receptor - used esp. for screening
PI	cncls. for activity as opiate agonists or antagonists
PS	Claim 1, Page 25-26; 49pp; English.
CC	hMOR cDNA was obtcd. from a human cerebral cortical cDNA library
CC	screened with fragments of a rat mu opiate receptor. Expression
CC	of hMOR in COS cells revealed high affinity recognition of the mu
CC	opiate specific ligand. Recombinant hMOR can be used to screen
CC	compounds for analgesic activity.
CC	Sequence 400 AA.

Query Match 68.2%; Score 1520; DB 14; Length 400;
Best Local Similarity 67.1%; Preg. No. 2.73e-127;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

MPERLH (TM)

Release 3.1A John F. Collins, BioComputing Research Unit.
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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Feb 17 11:17:17 2000; Maspar time 7.39 Seconds
Tabular output not generated. 517.015 Million cell updates/sec

Title: >US-08-455-683-12
Description: (1-295) from US08455683.pep
Perfect Score: 229
Sequence: 1 YTKMTATNIYIFNALADA.....NTVQDPAYLRIDGMNKPV 295

Scoring table: PAM 150
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 1:5A_COMB 2:5B_COMB 3:PCN9_COMB 4:backfiles1

Statistics: Mean 31.719; Variance 152.161; scale 0.208

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2123	95.2	380	1	US-08-149-Sequence 7, Applicatio	1.68e-175
2	2123	95.2	380	2	US-08-911-Sequence 7, Applicatio	1.88e-175
3	1990	89.3	378	2	US-08-514-Sequence 10, Applicatio	1.28e-163
4	1522	68.3	391	2	US-08-454-Sequence 3, Applicatio	6.69e-122
5	1522	68.3	400	3	PCT-US94-1Sequence 8, Applicatio	6.69e-122
6	1520	68.2	398	1	US-08-149-Sequence 5, Applicatio	1.01e-121
7	1520	68.2	398	2	US-08-911-Sequence 5, Applicatio	1.01e-121
8	1520	68.2	398	3	PCT-US94-1Sequence 2, Applicatio	1.01e-121
9	1452	65.1	367	2	US-08-454-Sequence 4, Applicatio	1.12e-115
10	1451	65.1	372	2	US-08-911-Sequence 6, Applicatio	1.37e-115
11	1451	65.1	372	1	US-08-149-Sequence 2, Applicatio	1.37e-115
12	1448	65.0	372	2	US-08-411-Sequence 2, Applicatio	2.53e-115
13	1448	65.0	372	2	US-08-411-Sequence 10, Applicati	2.53e-115
14	1426	64.0	398	2	US-08-514-Sequence 8, Applicatio	2.28e-113
15	1385	62.1	330	2	US-08-454-Sequence 5, Applicatio	9.99e-110
16	1345	60.3	367	2	US-08-454-Sequence 2, Applicatio	3.54e-106
17	1345	60.3	367	3	PCT-US94-1Sequence 17, Applicati	3.54e-106
18	1344	60.3	372	2	US-08-514-Sequence 9, Applicatio	4.35e-106
19	1335	59.9	367	1	US-08-149-Sequence 4, Applicatio	2.73e-105
20	1335	59.9	367	2	US-08-553-Sequence 4, Applicatio	2.73e-105
21	1335	59.9	367	2	US-08-514-Sequence 4, Applicatio	2.73e-105
22	1335	59.9	367	2	US-08-911-Sequence 4, Applicatio	2.73e-105
23	1230	55.2	367	2	US-08-514-Sequence 7, Applicatio	5.54e-96

24	1066	47.8	367	1	US-08-147-Sequence 2, Applicatio	1.75e-81
25	830	37.2	391	1	US-08-417-Sequence 4, Applicatio	1.01e-60
26	830	37.2	391	1	US-08-417-Sequence 14, Applicati	1.01e-60
27	830	37.2	391	1	US-08-417-Sequence 2, Applicatio	1.01e-60
28	830	37.2	391	1	US-07-816-Sequence 2, Applicatio	1.01e-60
29	830	37.2	391	1	US-08-411-Sequence 3, Applicatio	1.01e-60
30	788	35.4	369	2	US-08-411-Sequence 3, Applicatio	4.78e-57
31	785	35.2	369	1	US-07-816-Sequence 8, Applicatio	8.74e-57
32	785	35.2	369	1	US-08-417-Sequence 8, Applicatio	8.74e-57
33	780	35.0	369	1	US-08-417-Sequence 16, Applicati	2.39e-56
34	780	35.0	369	1	US-08-417-Sequence 6, Applicatio	2.39e-56
35	780	35.0	369	1	US-07-816-Sequence 6, Applicatio	2.39e-56
36	736	33.0	333	1	US-08-148-Sequence 4, Applicatio	1.66e-52
37	727	32.6	322	3	PCT-US93-0Sequence 75, Applicati	1.01e-51
38	727	32.6	322	1	US-08-118-Sequence 75, Applicati	1.01e-51
39	683	30.6	418	1	US-08-417-Sequence 10, Applicati	6.90e-48
40	683	30.6	418	1	US-07-816-Sequence 2, Applicatio	5.64e-46
41	661	29.7	328	1	US-08-148-Sequence 19, Applicati	1.12e-42
42	623	27.9	211	2	US-08-771-Sequence 19, Applicati	1.12e-42
43	623	27.9	211	1	US-07-915-Sequence 12, Applicati	1.34e-40
44	599	26.9	428	1	US-07-816-Sequence 12, Applicati	1.34e-40
45	599	26.9	428	1	US-08-417-Sequence 12, Applicati	1.34e-40

ALIGNMENTS

RESULT 1
ID US-08-149-093A-7 STANDARD; PRT; 380 AA.
XX
AC xxxxxx
XX
XX
DT
XX

Sequence 7, Application US/08149093A

Sequence 7, Application US/08149093A
Patent No. 5658783
GENERAL INFORMATION:

APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K
TITLE OF INVENTION: A NO. 5658783el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,093A
FILING DATE: 06-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5658783ban, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10358
CC FILING DATE: Concurrently herewith
CC CLASSIFICATION:
CC PRIORITY DATA:
CC APPLICATION NUMBER: 08/120,601
CC FILING DATE: 13 SEPTEMBER 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILSON, MARK B.
CC REGISTRATION NUMBER: 37,259
CC REFERENCE/DOCKET NUMBER: INDA005P--
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-5000
CC TELEFAX: (713) 789-2679
CC TELEX: 79-0924
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 400 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 400 AA; 44779 MW; 873826 CN;

Query Match 68.3%; Score 1522; DB 3; Length 400;
Best Local Similarity 67.1%; Pred. No. 6.69e-122;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db 98 YTKMKTATNIYIFNLADALATSTLPFQSVNVLMTGWPFGTILCKIVISIDYNNMFTSI 157
QY 1 YTKMKTATNIYIFNLADALATSTLPFQSVNVLMTGWPFGTILCKIVISIDYNNMFTSI 60

Db 158 FTLTMSVDRIYAVCHPVKALDFTPRNAKIIVNCNWLSSAIGLPVFMATTKYRG-S 216
QY 61 FTLTMSVDRIYAVCHPVKALDFTPRNAKIIVNCNWLSSAIGLPVFMATTKYRG-S 120

Db 217 -IDCTLFSSPTW-YWENLLKICVFIFAFVPIVLIIVCYTILMLRLKSVRLSGSKED 274
QY 121 VIECGLQFPDDYSWDLFMKICVFIFAFVPIVLIIVCYTILMLRLKSVRLSGSKED 180

Db 275 RNLRRIRMLVAVVAVFVVCWTPHIIYVILKALITIPETTFQIVSWHFCIALGYTNSLN 334
QY 181 XNLRIRITLVVAVFVVCWTPHIIYVILKALITIPETTFQIVSWHFCIALGYTNSLN 240

Db 335 PVLVAFDENFKRCFRFCPTSTNIEQQNSTRIQRNTRD 374
QY 241 PVLVAFDENFKRCFRFCPTSTNIEQQNSTRIQRNTRD 280

RESULT 6
ID US-08-149-093A-5 STANDARD; PRT; 398 AA.
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AC xxxxxx
XX
DT
XX
DE Sequence 5, Application US/08149093A
XX Sequence 5, Application US/08149093A
CC Patent No. 5658783
CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R
CC APPLICANT: Grandy, David K
CC TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific
CC TITLE OF INVENTION: Opioid Receptor Gene and Uses
CC NUMBER OF SEQUENCES: 7

CC CORRESPONDENCE ADDRESS:
CC ADDRESSES: Banner & Allegretti, Ltd.
CC STREET: 10 South Wacker Drive, Suite 3000
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/149,093A
CC FILING DATE: 06-NOV-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5658783nan, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,311
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-715-1000
CC TELEFAX: 312-715-1234
CC TELEX: 910-221-5317
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 398 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..398
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Rat Mu-Opioid Receptor"
CC SEQUENCE 398 AA; 44508 MW; 870781 CN;

Query Match 68.2%; Score 1520; DB 1; Length 398;
Best Local Similarity 65.7%; Pred. No. 1.01e-121;
Matches 190; Conservative 46; Mismatches 49; Indels 4; Gaps 4;

Db 96 YTKMKTATNIYIFNLADALATSTLPFQSVNVLMTGWPFGTILCKIVISIDYNNMFTSI 155
QY 1 YTKMKTATNIYIFNLADALATSTLPFQSVNVLMTGWPFGTILCKIVISIDYNNMFTSI 60

Db 156 FTLTMSVDRIYAVCHPVKALDFTPRNAKIIVNCNWLSSAIGLPVFMATTKYRG-S 214
QY 61 FTLTMSVDRIYAVCHPVKALDFTPRNAKIIVNCNWLSSAIGLPVFMATTKYRG-S 120

Db 215 -IDCTLFSSPTW-YWENLLKICVFIFAFVPIVLIIVCYTILMLRLKSVRLSGSKED 272
QY 121 VIECGLQFPDDYSWDLFMKICVFIFAFVPIVLIIVCYTILMLRLKSVRLSGSKED 180

Db 273 RNLRRIRMLVAVVAVFVVCWTPHIIYVILKALITIPETTFQIVSWHFCIALGYTNSLN 332
QY 181 XNLRIRITLVVAVFVVCWTPHIIYVILKALITIPETTFQIVSWHFCIALGYTNSLN 240

Db 333 PVLVAFDENFKRCFRFCPTSTNIEQQNSTRIQRNTRDHPSTANTVD 381
QY 241 PVLVAFDENFKRCFRFCPTSTNIEQQNSTRIQRNTRDHPSTANTVD 288

RESULT 7
ID US-08-911-245-5 STANDARD; PRT; 398 AA.
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AC xxxxxx
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DT
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DE Sequence 5, Application US/08911245
XX Sequence 5, Application US/08911245
CC Patent No. 5831067

CC GENERAL INFORMATION:
CC APPLICANT: Bunzow, James R
CC APPLICANT: Grandy, David K
CC TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
CC TITLE OF INVENTION: Opioid Receptor Gene and Uses
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Banner & Allegretti, Ltd.
CC STREET: 10 South Wacker Drive, Suite 3000
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/911,245
CC FILING DATE: 15-AUG-1997
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/149093
CC FILING DATE: 06-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: No. 5821067nan, Kevin E
CC REGISTRATION NUMBER: 35,303
CC REFERENCE/DOCKET NUMBER: 93,311
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-715-1000
CC TELEFAX: 312-715-1234
CC TELEX: 910-221-5317
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 398 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..398
CC OTHER INFORMATION: /label= Identifier
CC OTHER INFORMATION: /note= "Rat Mu-Opioid Receptor"
CC SEQUENCE 398 AA; 44508 MW; 870781 CN;

Query Match 68.2%; Score 1520; DB 2; Length 398;
Best Local Similarity 65.7%; Pred. No. 1.01e-121;
Matches 190; Conservative 46; Mismatches 49; Indels 4; Gaps 4;
Dbb 96 YTKWKTATNIYIFNLALADALATSTLPFSQVNYLMGTWPGTILCKIVISIDYNNMFTSI 155
Qy 1 YTKWKTATNIYIFNLALADALATSTLPFSQVNYLMGTWPGTILCKIVISIDYNNMFTSI 60
Dbb 156 FTLCTMSVDRIYACHPVKALDFTPRNAKIVNVCNMLSSAIGLPMVFMATTKYRQ-S 214
Qy 61 FTLTMSVDRIYACHPVKALDFTPRNAKIVNVCNMLSSAIGLPMVFMATTKYRQ-S 120
Dbb 215 -IDCTLFSPHTW-YWENLLKICVFIFAFIPVLIIVCYGLMILRLKSVRLSGSKEKD 272
Qy 121 VIECLOPDDDDYSWDLFMKICVFIFAFIPVLIIVCYGLMILRLKSVRLSGSKEKD 180
Dbb 273 RNLRRITRMVLVVAIVFVCTPHIYIIVKALITPTTFQTVSWHFCIALGTNSCLN 332
Qy 181 XNLRITRLVLVVAIVFVCTPHIYIIVKALITPTTFQTVSWHFCIALGTNSCLN 240
Dbb 333 PVLYAFLDENKRCFRFCPTSTTIEQONSTRVQNTREHPSTANTVD 381
Qy 241 PILYAFLDENKRCFRFCPTSTTIEQONSTRVQNTREHPSTANTVD 288
RESULT 8
ID PCI-US94-10358-2 STANDARD; PRI: 398 AA.

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AC
XX
DT
XX
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DE
XX
CC Sequence 2, Application PC/TUS9410358
CC Sequence 2, Application PC/TUS9410358
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENT IN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10358
CC FILING DATE: Concurrently herewith
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/120.601
CC FILING DATE: 13 SEPTEMBER 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILSON, MARK B.
CC REGISTRATION NUMBER: 37,259
CC REFERENCE/DOCKET NUMBER: INDA00SP--
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-3000
CC TELEFAX: (713) 789-2679
CC TELEX: 79-0924
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 398 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 398 AA; 44508 MW; 870781 CN;
Query Match 68.2%; Score 1520; DB 3; Length 398;
Best Local Similarity 65.7%; Pred. No. 1.01e-121;
Matches 190; Conservative 46; Mismatches 49; Indels 4; Gaps 4;
Dbb 96 YTKWKTATNIYIFNLALADALATSTLPFSQVNYLMGTWPGTILCKIVISIDYNNMFTSI 155
Qy 1 YTKWKTATNIYIFNLALADALATSTLPFSQVNYLMGTWPGTILCKIVISIDYNNMFTSI 60
Dbb 156 FTLCTMSVDRIYACHPVKALDFTPRNAKIVNVCNMLSSAIGLPMVFMATTKYRQ-S 214
Qy 61 FTLTMSVDRIYACHPVKALDFTPRNAKIVNVCNMLSSAIGLPMVFMATTKYRQ-S 120
Dbb 215 -IDCTLFSPHTW-YWENLLKICVFIFAFIPVLIIVCYGLMILRLKSVRLSGSKEKD 272
Qy 121 VIECLOPDDDDYSWDLFMKICVFIFAFIPVLIIVCYGLMILRLKSVRLSGSKEKD 180
Dbb 273 RNLRRITRMVLVVAIVFVCTPHIYIIVKALITPTTFQTVSWHFCIALGTNSCLN 332
Qy 181 XNLRITRLVLVVAIVFVCTPHIYIIVKALITPTTFQTVSWHFCIALGTNSCLN 240
Dbb 333 PVLYAFLDENKRCFRFCPTSTTIEQONSTRVQNTREHPSTANTVD 381
Qy 241 PILYAFLDENKRCFRFCPTSTTIEQONSTRVQNTREHPSTANTVD 288
RESULT 9

Search completed: Thu Feb 17 11:17:26 2000
Job time : 9 secs.

(TM)

Result No.	Query		DB	ID	Description	Pred. No.	
	Score	Match Length					
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2	2192	98.3	380	2	I57005	opioid receptor kappa	0.00e+00
3	2157	96.8	380	2	A53259	kappa opioid receptor	0.00e+00
4	2136	95.8	380	2	A48227	kappa opioid receptor	0.00e+00
5	2132	95.6	380	2	S36143	kappa opioid receptor	0.00e+00
6	2114	94.8	380	2	JC2434	kappa-opioid receptor	0.00e+00
7	1524	68.4	398	2	A57510	mu opioid receptor -	8.97e-243
8	1523	68.3	373	2	JE0087	delta opioid receptor	1.36e-242
9	1522	68.3	400	2	I56533	opioid receptor mu	2.06e-242
10	1520	68.2	392	2	S65593	opioid receptor mu va	4.75e-242
11	1520	68.2	398	2	I56517	mu-opioid receptor -	4.75e-242
12	1505	67.5	398	2	I56504	mu opioid receptor -	2.45e-239
13	1458	65.4	372	2	I38657	delta opiate receptor	7.65e-231
14	1458	65.4	372	2	I38532	delta opioid receptor	7.65e-231
15	1452	65.1	372	2	S34592	delta opioid receptor	9.28e-230
16	1448	65.0	372	2	B48227	delta opioid receptor	4.90e-229
17	1345	60.3	367	2	I56520	G protein-coupled rec	1.86e-210
18	1343	60.3	367	2	JC2421	opioid receptor homol	4.27e-210
19	1342	60.2	367	2	I49022	K3 opiate receptor -	6.47e-210
20	1331	59.7	370	2	S43067	orphan opioid recepto	6.19e-208
21	830	37.2	331	2	A39297	somatostatin receptor	1.86e-118
22	830	37.2	331	2	C41795	somatostatin receptor	1.66e-118
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Db 147 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLSSVSGTSAIVLGSTKREDVD 206
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Qy 121 VTECSLQFPDDYSWDLFMKICVFIFAFVPLVLIIVCYTIMLRLKSVRLSSGREKD 180
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Qy 181 XNLRITRLVLVAVFVVCWTPPIHIFILVEALGSTSHSTAALSYFYFCIALGYTNSSLN 240
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Db 327 PILYAFLDENKRCRDFCFPLKMXMERQSTSRVNTVQDPAYLRDIDGM-NKPV 380
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Qy 241 PILYAFLDENKRCRDFCFPLKMXMERQSTSRVNTVQDPAYLRDIDGMNKPV 295
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RESULT 2 157005 #type complete
ENTRY opiod receptor kappa-1 - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 29-Aug-1997
ACCESSIONS 157005
REFERENCE 157005
#authors Zhu, J.; Chen, C.; Xue, J.
#journal Life Sci. (1995) 56:201-207
#title Cloning of a human kappa. opiod receptor from the brain.
#accession 157005
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-380 #label RES
#cross-references GB:L37362; NID:g722617; PID:g722618
GENETICS
#gene GDB:OPR1; KOR
#cross-references GDB:L32651; OMIM:165196
#map_position 8q11.2-8q11.2
SUMMARY #length 380 #molecular-weight 42645 #checksum 8302

Query Match 98.3%; Score 2192; DB 2; Length 380;
Best Local Similarity 97.6%; Pred. No. 0.00e+00;
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 YTKMTATNIYIFNLADALVTTMPFQSTVYLMNSWPFGLCKIIVISIDYNNFTSI 146
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Db 147 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLSSVSGTSAIVLGSTKREDVD 206
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Qy 181 XNLRITRLVLVAVFVVCWTPPIHIFILVEALGSTSHSTAALSYFYFCIALGYTNSSLN 240
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Db 327 PILYAFLDENKRCRDFCFPLKMXMERQSTSRVNTVQDPAYLRDIDGM-NKPV 380
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Qy 241 PILYAFLDENKRCRDFCFPLKMXMERQSTSRVNTVQDPAYLRDIDGMNKPV 295
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RESULT 3
ENTRY A55259
TITLE kappa opiod receptor - guinea pig
ALTERNATE_NAMES dynorphin receptor
ORGANISM #formal_name Cavia porcellus #common_name guinea pig
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
10-Sep-1997
ACCESSIONS A55259
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REFERENCE A55259
#authors Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten,
M.T.; Goldstein, A.; Watson, S.J.; Akil, H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:3779-3783
#title Primary structure and functional expression of a guinea pig
kappa opiod (dynorphin) receptor.
#accession A55259
#status preliminary
#molecule_type mRNA
#residues 1-380 #label XIE
#cross-references GB:U04092; NID:g476106; PID:g476107
KEYWORDS transmembrane protein
SUMMARY #length 380 #molecular-weight 42736 #checksum 7081

Query Match 96.8%; Score 2157; DB 2; Length 380;
Best Local Similarity 94.6%; Pred. No. 0.00e+00;
Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

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Qy 1 YTKMTATNIYIFNLADALVTTMPFQSTVYLMNSWPFGLCKIIVISIDYNNFTSI 60
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Db 147 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLSSVSGTSAIVLGSTKREDVD 206
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Qy 241 PILYAFLDENKRCRDFCFPLKMXMERQSTSRVNTVQDPAYLRDIDGMNKPV 295
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RESULT 4
ENTRY A48227
TITLE kappa opiod receptor 1 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 26-May-1994 #sequence_revision 26-May-1994 #text_change
10-Sep-1997
ACCESSIONS A48227; JC4138
REFERENCE A48227
#authors Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.;
Reisine, T.; Bell, G.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740
#title Cloning and functional comparison of kappa and delta opiod
receptors from mouse brain.
#cross-references MUID:93342064
#accession A48227
#status preliminary
#molecule_type mRNA
#residues 1-380 #label YAS
#cross-references GB:L11065; NID:g348248; PID:g348249
REFERENCE JC4138
#authors Liu, H.C.; Lu, S.; Augustin, L.B.; Felsheim, R.F.; Chen,
H.C.; Loh, H.H.; Wei, L.N.
#journal Biochem. Biophys. Res. Commun. (1995) 209:639-647
#title Cloning and promoter mapping of mouse kappa opiod receptor
gene.
#cross-references MUID:95251663
#accession JC4138
#molecule_type mRNA
#residues 1-380 #label LIU
#note The authors translated the codon CAG for residue 365 as
Glu
COMMENT This receptor exists in different areas of the central and
peripheral nervous systems, and mediates many physiological and
pharmacological effects of opiates and opiod compounds.
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GENETICS

#gene

KEYWORDS

kor
 brain; G protein-coupled receptor; glycoprotein; opioid peptide; phosphoprotein; transmembrane protein
 #length 380 #molecular-weight 42652 #checksum 9937

SUMMARY

Query Match 95.8%; Score 2136; DB 2; Length 380;
 Best Local Similarity 92.9%; Pred. No. 0.00e+00;
 Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 87 YTKMTATNIYIFNLADALVTTTTPFQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 146
 QY 1 YTKMTATNIYIFNLADALVTTTTPFQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 60
 Db 147 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLASSVGSIAVLGKTKVREDVD 206
 QY 61 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLSSVGSIAVLGKTKVREDVD 120
 Db 207 VIECSLPDDDEYSWDLFMKICVFVAFVPLVLIIVCYTIMLRLKSVRLSSGREKD 266
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 Db 267 RNLRTITLVLVWVAVFICWTPPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 326
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 Db 327 PVLVAFLDENFKRCDFCFPIKXMEROSINRVRNTVQDPASMRDVGGM-NKPV 380
 QY 241 PVLVAFLDENFKRCDFCFPIKXMERXSTSRVRNTVQDPAYLREIDGMNKPV 295

RESULT

ENTRY S36143 #type complete
 TITLE kappa opioid receptor - rat
 ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
 DATE 10-Dec-1993 #sequence_revision 19-Oct-1995 #text_change 29-Jan-1999
 ACCESSIONS S36143; S38825; S36102; S39015; A48789
 REFERENCE S36143
 #authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, K.
 #journal FEBS Lett. (1993) 330:77-80
 #title cDNA cloning and pharmacological characterization of an opioid receptor with high affinities for kappa-subtype-selective ligands.
 #cross-references MUID:93380575

#accession S36143
 #status Preliminary
 #molecule_type mRNA
 #residues 1-380 #label NIS
 #cross-references GB:D16534; NID:g409390; PID:d1004487; PID:g415310
 REFERENCE S38825
 #authors Chen, Y.; Mestek, A.; Liu, J.; Yu, L.
 #journal Biochem. J. (1993) 295:625-628
 #title Molecular cloning of a rat kappa opioid receptor reveals sequence similarities to the mu and delta opioid receptors.
 #accession S38825
 #status Preliminary
 #molecule_type mRNA
 #residues 1-380 #label CHE
 #cross-references GB:L22001; NID:g409235; PID:g409237
 REFERENCE S36102
 #authors Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko, S.; Sato, M.
 #journal FEBS Lett. (1993) 329:291-295
 #title Cloning and expression of a cDNA for the rat kappa-opioid receptor.
 #cross-references MUID:93374033
 #accession S36102
 #molecule_type mRNA
 #residues 1-41, 'L' 43-380 #label MIN
 #cross-references GB:D16829; NID:g404115; PID:d1004628; PID:g404116

REFERENCE

#authors Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.K.; Ashby,

#journal

#title

#accession S39015

#molecule_type mRNA

#residues 1-344, 'Y', 346-380 #label LIS

REFERENCE A48789

#authors Meng, F.; Xie, G.

#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958

#title Cloning and pharmacological characterization of a rat kappa opioid receptor.

#cross-references MUID:94052210

#accession A48789

#status Preliminary; translated from GB/EMBL/DBJ

#molecule_type mRNA

#residues 1-380 #label RES

#cross-references EMBL:U00442; NID:g403486; PID:g403487

KEYWORDS G protein-coupled receptor; transmembrane protein

SUMMARY #length 380 #molecular-weight 42688 #checksum 9972

Query Match

Best Local Similarity 92.5%; Pred. No. 0.00e+00;

Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMTATNIYIFNLADALVTTTTPFQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 146
 QY 1 YTKMTATNIYIFNLADALVTTTTPFQSAVYLMNSWPFQGVLCIKIVISIDYNNFTSI 60
 Db 147 FTLTMSVDRIYAVCHPVKALDFRPLKAKIINICIWLLASSVGSIAVLGKTKVREDVD 206
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 QY 181 RNLRTITLVLVWVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSSLN 240
 Db 327 PVLVAFLDENFKRCDFCFPIKXMEROSINRVRNTVQDPASMRDVGGM-NKPV 380
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RESULT

ENTRY JC2434 #type complete
 TITLE kappa-opioid receptor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 05-Apr-1995
 ACCESSIONS JC2434
 REFERENCE JC2434
 #authors Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.
 #journal Biochem. Biophys. Res. Commun. (1994) 205:1353-1357
 #title Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor and an opioid receptor homologue (MOR-C).
 #cross-references MUID:95100967

#accession JC2434

#molecule_type mRNA

#residues 1-380 #label NIS

#cross-references DBJ:D31663

GENETICS

#map_position 1A2-3

#introns 86/2; 204/1

KEYWORDS receptor

SUMMARY

#length 380 #molecular-weight 42630 #checksum 9705

Query Match

Best Local Similarity 94.8%; Score 2114; DB 2; Length 380;

Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

```

Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;
Db 87 YTKMTATNIYFNALADALVTTMPFQSAVYLNMSWPFQSVLCKIVISIDYNNFTSI 146
      |||||
QY 1 YTKMTATNIYFNALADALVTTMPFQSTVYLNMSWPFQSVLCKIVISIDYNNFTSI 60
      |||||
Db 147 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWILSSVSGISAVILGCTKVRD 206
      |||||
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWILSSVSGISAVILGCTKVRD 120
      |||||
Db 207 VIECCLQPDDEYSWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKXVRLSSGSK 266
      |||||
QY 121 VIECCLQPDDEYSWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKXVRLSSGSK 180
      |||||
Db 267 RNLRTITRLVAVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYFICIALGY 326
      |||||
QY 181 XNLRITRLVAVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYFICIALGY 240
      |||||
Db 327 PVLYAFDENFKRCRDFCFPLKMXERQSTNRVNTVQDPASMRDVGKM-NKPV 380
      |||||
QY 241 PILYAFDENFKRCRDFCFPLKMXERXSTSRVNTVQDPAYLREIDGMNKPV 295
      |||||

RESULT 7
ENTRY A57510 #type complete
TITLE mu opioid receptor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change
07-Nov-1997
ACCESSIONS A57510; I48665; S66513; I49300
REFERENCE A57510
#authors Kaufman, D.L.; Keith Jr., D.B.; Anton, B.; Tian, J.;
          Magendzo, K.; Newman, D.; Tran, T.H.; Lee, D.S.; Wen, C.;
          Xia, Y.R.; Lusis, A.J.; Evans, C.J.
#journal J. Biol. Chem. (1995) 270:15977-15983
#title Characterization of the murine mu opioid receptor gene.
#accession A57510
#status nucleic acid sequence not shown
##residues 1-398 ##label KAU
##cross-references GB:U19380
REFERENCE I48665
#authors Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh,
          H.H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9081-9085
#title Genomic structure analysis of promoter sequence of a mouse mu
          opioid receptor gene.
#cross-references MUID:94377496
#accession I48665
#status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-398 ##label RES
##cross-references EMBL:U10561; NID:g555696; PID:g565069
REFERENCE I49300
#authors Rossi, G.C.; Pap, Y.X.; Brown, G.P.; Pasternak, G.W.
#journal F.E.B.S. Lett. (1995) 369:192-196
#title Antisense mapping the MOR-1 opioid receptor: evidence for
          alternative splicing and a novel morphine-6
          beta-glucuronide receptor.
#cross-references MUID:95377399
#accession S66513
#status nucleic acid sequence not shown; translation not shown
##molecule_type mRNA
##residues 1-398 ##label ROS
##cross-references EMBL:U26915; NID:g1055230; PID:g1055231
#note the nucleotide sequence was submitted to the EMBL Data
      Library, November 1995

GENETICS MOR-1
#gene 95/2; 213/1; 386/3
#introns alternative splicing; G protein-coupled receptor;
#keywords glycoprotein; transmembrane protein
SUMMARY #length 398 #molecular-weight 44421 #checksum 8164

```

```

Query Match 68.4%; Score 1524; DB 2; Length 398;
Best Local Similarity 65.7%; Pred. No. 8,97e-243;
Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;
Db 96 YTKMTATNIYFNALADALATSTLPFQSNVYLMGTWPGNLCIKIVISIDYNNFTSI 155
      |||||
QY 1 YTKMTATNIYFNALADALVTTMPFQSTVYLNMSWPFQSVLCKIVISIDYNNFTSI 60
      |||||
Db 156 FTLTMSVDRIYAVCHPVKALDFRTPKAKIYNVCNWLSSAIGLVPFMATIKYRQ-S 214
      |||||
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWILSSVSGISAVILGCTKVRD 120
      |||||
Db 215 -IDCPLITSHPTW-YWENLLKICVFIFAFVPIVLIIVCYTLMILRLKXVRLSSGSK 272
      |||||
QY 121 VIECCLQPDDEYSWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKXVRLSSGSK 180
      |||||
Db 273 RNLRTITRLVAVVAVFVVCWTPPIHIVYIKALIIPTTFTQVSWHFICIALGY 332
      |||||
QY 181 XNLRITRLVAVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYFICIALGY 240
      |||||
Db 333 PVLYAFDENFKRCRDFCFPLKMXERQSTNRVNTVQDPASMRDVGKM-NKPV 381
      |||||
QY 241 PILYAFDENFKRCRDFCFPLKMXERXSTSRVNTVQDPAYLREID 288
      |||||

RESULT 8
ENTRY JE0087 #type complete
TITLE delta opioid receptor - Zebrafish
ORGANISM #formal_name Danio rerio
DATE 14-May-1998 #sequence_revision 29-May-1998 #text_change
24-Sep-1998
ACCESSIONS JE0087
REFERENCE JE0087
#authors Barriallo, A.; Gonzalez-Sarmiento, R.; Porteros, A.;
          Garcia-Isidoro, M.; Rodriguez, R.E.
#journal Biochem. Biophys. Res. Commun. (1998) 245:544-548
#title Cloning, molecular characterization, and distribution of a gene
          homologous to delta opioid receptor from zebrafish (Danio
          rerio).
#accession JE0087
##molecule_type mRNA
##residues 1-373 ##label BAR
##cross-references EMBL:AJ001596; NID:g2739230; PID:e1217996;
          PID:g2739231
COMMENT This protein mediates the effects of morphine and the related
          drugs, and is the targets of endogenous opioid peptides.
KEYWORDS glycoprotein
FEATURE 21,37
#binding_site carbohydrate (Asn) (covalent) #status
          predicted
SUMMARY #length 373 #molecular-weight 42520 #checksum 674
Query Match 68.3%; Score 1523; DB 2; Length 373;
Best Local Similarity 66.0%; Pred. No. 1,36e-242;
Matches 186; Conservative 52; Mismatches 40; Indels 4; Gaps 4;
Db 80 YTKMTATNIYFNALADALATSTLPFQSTVYLNMSWPFQSVLCKIVISIDYNNFTSI 139
      |||||
QY 1 YTKMTATNIYFNALADALVTTMPFQSTVYLNMSWPFQSVLCKIVISIDYNNFTSI 60
      |||||
Db 140 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINVCNWLSSVSGISAVILGCTKVRD 199
      |||||
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWILSSVSGISAVILGCTKVRD 120
      |||||
Db 200 TV-CMLKFPDDEW-YDWTVKICVFIFAFVPIVLIIVCYTLMILRLKXVRLSSGSK 257
      |||||
QY 121 VIECCLQPDDEYSWDLFMKICVFIFAFVPIVLIIVCYTLMILRLKXVRLSSGSK 180
      |||||
Db 258 RNLRTITRLVAVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYFICIALGY 316
      |||||
QY 181 XNLRITRLVAVVAVFVVCWTPPIHIFILVEALGSTSHSTAALSSYFICIALGY 239
      |||||

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```

Db 317 NPVLYAFDENKRCRDFCIPETRADQSNLNARNATREP 358
      :::::::::::::::::::::::  :::::
QY 240 NPVLYAFDENKRCRDFCIPPLKXMXERXSTSRVNVQDP 281

```

```

RESDLI 9
ENTRY
  TITLE      #type complete
  ALTERNATE_NAMES MORI protein; opioid receptor mu
  ORGANISM   Homo sapiens
  DATE       02-Jul-1996
  sequence_revision 02-Jul-1996
  #text_change

ACCESSIONS I56553; A38991; S41075; S51215
REFERENCE
  #authors   Mestek, A.; Hurley, J.H.; Bye, L.S.; Campbell, A.D.; Chen, Y.; Tian, M.; Liu, J.; Schulman, H.; Yu, L.
  #journal   J. Neurosci. (1995) 15:2396-2406
  #title     The human mu opioid receptor: modulation of functional desensitization by calcium/calmodulin-dependent protein kinase and protein kinase C.
  #cross-references MUID:95198115
  #accession I56553
  ##status   nucleic acid sequence not shown; translated from GB/EMBL/DBJ

  ##molecule_type mRNA
  ##residues 1-400
  ##label RES
  ##cross-references GB:L29301; NID:g459831; PID:g459832
REFERENCE
  #authors   Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.R.
  #submission submitted to GenBank, August 1994
  #accession A38991
  ##status   translated from GB/EMBL/DBJ
  ##molecule_type mRNA
  ##residues 1-50, 'N', 52-233, 'V', 235-400
  ##label WAN
  ##cross-references GB:L25119; NID:g452072; PID:g452073
  #accession S41075
REFERENCE
  #authors   Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.R.
  #journal   FEBS Lett. (1994) 338:217-222
  #title     Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment.
  #cross-references MUID:94139928
  #accession S41075
  ##status   nucleic acid sequence not shown
  ##molecule_type mRNA
  ##residues 1-50, 'N', 52-400
  ##label WA2
REFERENCE
  #authors   Bare, L.A.; Masson, E.; Yang, D.
  #journal   FEBS Lett. (1994) 354:213-216
  #title     Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.
  #cross-references MUID:95046336
  #accession S51215
  ##status   preliminary
  ##molecule_type mRNA
  ##residues 387-400
  ##label BAR
GENERIC5
  #gene      GDB:OPRM1
  ##cross-references GDB:137216; OMIM:600018
  #map_position 6q24-6q25
KEYWORDS
  G protein-coupled receptor; glycoprotein; transmembrane protein
FEATURE
  73-96
  107-132
  144-165
  180-208
  236-257
  293-304
  323-342
  9,12,33,40,48
  #domain transmembrane
  #status predicted
  #label TM1\
  #domain transmembrane
  #status predicted
  #label TM2\
  #domain transmembrane
  #status predicted
  #label TM3\
  #domain transmembrane
  #status predicted
  #label TM4\
  #domain transmembrane
  #status predicted
  #label TM5\
  #domain transmembrane
  #status predicted
  #label TM6\
  #domain transmembrane
  #status predicted
  #label TM7\
  #binding_site carbohydrate (Asn) (covalent)
  #status predicted

```

```

SUMMARY      #length 400  #molecular-weight 44779  #checksum 3741

Query Match      68.3%; Score 1522; DB 2: Length 400;
Best Local Similarity 67.1%; Pred. No. 2.06e-242;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db 98 YTKMKTATNIYIFNLADALATLTLPFQSVNYLMGTWPFGLTICKIVISIDYNNFTSI 157
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1 YTKMKTATNIYIFNLADALVITITPFQSTVYLMNSWPGDVLCIKIVISIDYNNFTSI 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 158 PTLCTMSVDRIYAVCHPVKALDPTPRNAKIINVCNWILSSAIGLPWFMTATKYQG-S 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 FTLMMSVDRIYAVCHPEVKALDFTPLKAIINICWILSSVSGISAIVLGGVKVEDVD 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 217 -IDCTLTFSPHTW-YWENLLKICVFIAFTMPVLITVCYGLMILRLKSVMLSGSKED 274
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 121 VTECLQFPDDTSWDLFWKLCVTFAFVPLVLIITVYITMLRLKXVRLSSGREKD 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 275 RNLRIITRLVWVAVFVQCTPIHIYVILKALVITPETFTQVSHFCIALGYTNKSN 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 181 XNLRRIITRLVWVAVFVQCTPIHIFILVEALGSHSTAALSSYFFCIALGYTNSSLN 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 335 PVLVAFIDENFKCFREFCIPTSSTNEQONSTRONTKD 374
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 241 PVLVAFIDENFKCFRCDFCFPLKXMXRSTSVRNTVD 280
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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RESULT      10
ENTRY
  TITLE      S65693 #type complete
  ORGANISM   oploid receptor mu variant MORIA - human
  DATE       12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
              10-Sep-1997
ACCESSIONS
  S65693; S51216
REFERENCE
  #authors   Bare, L.A.; Mansson, E.; Yang, D.
  #submission submitted to the EMBL Data Library, July 1994
  #description Expression of two variants of the human mu oploid receptor
              mRNA in SK-N-SH cells and human brain.
  #accession S65693
              ##molecule_type mRNA
              ##residues 1-392 ##label BAR
              ##cross-references EMBL:U12569; NID:g607911; PID:g607912
REFERENCE
  S51215
  #authors   Bare, L.A.; Mansson, E.; Yang, D.
  #journal   FEBS Lett. (1994) 354:213-216
  #title      Expression of two variants of the human mu oploid receptor
              mRNA in SK-N-SH cells and human brain.
  #cross-references MUID:95046336

```

```

SUMMARY      387-392 #label BAW
              #length 392 #molecular-weight 43939 #checksum 6977

Query Match      68.2%; Score 1520; DB 2; Length 392;
Best Local Similarity 67.1%; Pred. No. 4,756-242;
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;

Db 98 YTKMKATATNIYFNALADALATSLPFQSVANVLMGTWPFGLCKIVISIDYYNMFSTI 157
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 1 YTKMKATATNIYFNALADALVITTMFQSTVYLMKNSVPFGDVLCKIVISIDYYNMFSTI 60

Db 158 FTLTMSVDVRYIACVCPVKALDERTPRNAKIINVCNWLSSAIGLPVNFATKYKQG-S 216
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 61 FTLTMSVDVRYIACVCPVKALDERPLRAKIIINICLWLLSSVGVSAIVLGATKYKQVEDV 120

Db 217 -DCILTFSPHPW- TWENLLKTCVFIEFAPVPLIITVCYGLMILRLKSVRMLSGSKKD 274
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 121 VIECCIQFPDDDDYSWMDLFMKICVEIFAPVPLIIVCYTLMLRLKXVRLSSGSKKD 180

Db 275 RNLRITRRLVAVVAIVFCWTPPIHYYIKALVITPTTQTQVSWHFCIALGNTNSCLN 334
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 181 XNLRITRRLVAVVAIVFCWTPPIHIFILVEALGETSTAAALSSYYFCIALGNTNSLN 240

```

```

#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10230-10234
#title Mu opiate receptor: cDNA cloning and expression.
#cross-references MUID:94052137
#accession A48799
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-244, 'V' 246-398 #label WAN
##cross-references GB:I20684; NID:g409149; PID:g409150
REFERENCE I58154
#authors Thompson, R.C.; Mansour, A.; Akil, H.; Watson, J.S.
#journal Neuron (1993) 11:903-913
#title Cloning and pharmacological characterization of a rat mu
          opiod receptor.
#cross-references MUID:94059560
#accession I58154
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-244, 'V' 246-398 #label THO
##cross-references GB:I22455; NID:g437671; PID:g437672
GENETICS
#gene MUOR1
KEYWORDS
SUMMARY
          length 398 #molecular-weight 44508 #checksum 8374
          58.2%; Score 1520; DB 2; Length 398;
          Best Local Similarity 65.7%; Pred. No. 4.75e-242; Indels 4; Gaps 4;
          Matches 190; Conservative 46; Mismatches 49;

Db 96 YTKWKTATNYIENLADALATSTILPFSQVNYLMGTPFGTILCKIVISIDYNNFTSI 155
QY 1 YTKWKTATNYIENLADALVTTTFPQSTVYLMNSWPGDVLCKIVISIDYNNFTSI 60
      |||||
Db 156 FTLCSTSDRYIAVCHPVKALDFTFPNKAIVNVCNWILSSAIGLPVPMWATKYRQG-S 214
QY 61 FTLTMSVDRYIAVCHPVKALDFTPLKAKIINICWLLSSVSGISAIVLGGTKVEDVD 120
      |||||
Db 215 -IDCTLFSPTW-YWENLKICVFFAFTMPILLITVCGLMLRLKSVMLSGSKED 272
QY 121 VIECGLFPDDYSWMDLKKICVFFAFVPIVLIIVCYTLMRLKXVLLSGSKED 180
      |||||
Db 273 RNLRRIRFVLVVAVFVFCWTPTHYIVIAKILITPETFQVSWHFICIALGYTNSCLN 332
QY 181 XNLRIRFVLVVAVFVFCWTPTHIFILVEALGSGSHSTAALSSYFICIALGYTNSLN 240
      |||||
Db 333 PLYAYFLDENKRCFRFCFICSTSTIEQQNSTVRONTREHPSTANTVD 381
QY 241 PLYAYFLDENKRCFRFCFPLKMXMERXSTSRV-NIVODPAYLREID 288
      |||||

RESULT 12
ENTRY I56504 #type complete
TITLE mu opiod receptor - rat
ORGANISM #formal name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
      26-Jul-1996
ACCESSIONS I56504
REFERENCE I56504
#authors Zastawny, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos,
          J.; Briones-Urbina, R.; O'Dowd, B.F.
#journal J. Neurochem. (1994) 62:2099-2105
#title Cloning, characterization, and distribution of a mu-opioid
          receptor in rat brain.
#cross-references MUID:94246380
#accession I56504
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-398 #label RES
##cross-references EMBL:U35424; NID:gl017731; PID:gl017732
          length 398 #molecular-weight 44403 #checksum 8604
SUMMARY
          length 398; Score 1505; DB 2; Length 398;
          Best Local Similarity 67.5%; Pred. No. 2.45e-239;
          Matches 190; Conservative 45; Mismatches 50; Indels 4; Gaps 4;

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DATE	29-May-1998	#sequence_revision	29-May-1998	#text_change
ACCESSIONS	I38532			
REFERENCE	I38532			
#authors	Knapp, R.J.; Malatynska, E.; Fang, L.; Xiaoping, L.; Nguyen, M.; Santoro, G.; Varga, E.V.; Hruby, V.O.; Roeske, W.R.; Yamamura, H.I.			
#journal	Life Sci. (1994) 54:PL463-PL469			
#title	Identification of a human delta opioid receptor: Cloning and expression.			
#cross-references	MUID:94260835			
#accession	I38532			
#status	preliminary; translated from GB/EMBL/DDBJ			
#molecule_type	mRNA			
#residues	1-372	#label	RES	
#cross-references	EMBL:U07882; NID:g497313; PID:g497314			
SUMMARY	#length 372	#molecular-weight	40450	#checksum 2484
Query Match	65.4%;	Score	1458;	DB 2; Length 372;
Best Local Similarity	69.2%;	Pred. No.	7.65e-231;	
Matches	180;	Conservative	43;	Mismatches 33; Indels 4; Gaps 4;
Db	77 YTKMKTATNIYINFLADALANTSTLFFQSAYKLYMETWPEGLCKAVLSIDYNNMFSI	136		
QY	1 YTKMKTATNIYINFLADALANTSTLFFQSTVYLMNSWFGVCKIVISIDYNNMFSI	60		
Db	137 FTLTMSVDRIYAVCHPVKALDFTFAKAKLINICIWLASGVGVIMVAVTRPRDGA-	195		
QY	61 FTLTMSVDRIYAVCHPVKALDFTFIPLKAKINICIWLLSSVGSIAVLGKTKVEDVD	120		
Db	196 VV-CMLQFPSPW-YWDTVKICVFPAFWPILITVYGLMLRLRSVRLLSGSKKD	253		
QY	121 VIECGLQFPDDY-SWMDLFKICVFFAFVPIVLIIVCTYMLRLKXVRLLSGSKKD	180		
Db	254 RSLRRIIRMLVWVGAVCWABTHFVVTWLVDRDPLVWALHLCIALGVANSSL	313		
QY	181 XNLRIRILVWVAVFVVCWTFIHIFILVRLGSTSHSTA-ALSSYFICIALGYTNSSL	239		
Db	314 NPVIYAFLDENFKRCFRLC	333		
QY	240 NPVIYAFLDENFKRCFDFC	259		
RESULT	15			
ENTRY	S34592	#type	complete	
TITLE	delta opioid receptor - rat			
ORGANISM	#formal_name Rattus norvegicus	#common_name	Norway rat	
DATE	10-Dec-1993	#sequence_revision	10-Nov-1995	#text_change
ACCESSIONS	S34592			
REFERENCE	S34592			
#authors	Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.			
#journal	FEBS Lett. (1993) 327:311-314			
#title	Primary structures and expression from cDNAs of rat opioid receptor delta- and mu-subtypes.			
#cross-references	MUID:93351652			
#accession	S34592			
#molecule_type	mRNA			
#residues	1-372	#label	FUK	
#cross-references	GB:D16348; NID:g391864; PID:d1004367; PID:g391865			
REFERENCE	I36571			
#authors	Aboud, M.E.			
#journal	J. Neurosci. Res. (1994) 27:714-719			
#title	Molecular cloning and expression of a rat delta opioid receptor from rat brain.			
#accession	I36571			
#status	preliminary; translated from GB/EMBL/DDBJ			
#molecule_type	mRNA			
#residues	1-372	#label	RES	
#cross-references	EMBL:U00475; NID:g403488; PID:g514211			
GENETICS	dorl			
KEYWORDS	G protein-coupled receptor; transmembrane protein			

SUMMARY #length 372 #molecular-weight 40449 #checksum 2221

Query Match 65.1%; Score 1452; DB 2; Length 372;
Best Local Similarity 68.8%; Pred. No. 9,28e-230;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

Db 77 YTKLKTATNIYIFNLALADALATLTPFQSAKYLMTWPFGEELCKAVLSIDYNNMFTSI 136
Qy 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPFGEVLCKIVISIDYNNMFTSI 60

Db 137 FTLTMSVDRIYVCHPVKALDERTPAKALINICIMVLASSGVPIVMMAVIOPRGA- 195
Qy 61 FTLTMSVDRIYVCHPVKALDERTPAKALINICIMVLSSVGSALVGGTKVREDVD 120

Db 196 VV-CTLQPPSPSW-YWDEVTXICVLEFAFVVPILIIITVCYIGIMLRLRSVRLLSGSKED 253
Qy 121 VIECCLQFPDDDYSWWDLFMKICVFIFAFVIPVLIIIVCYTILMLRLKXVRLSGSREKD 180

Db 254 RSLRRTIRMLVYVVGAFVVCWAPIHIFVIVWTLVDINRDPVLVVAALHLCIALGYANSSL 313
Qy 181 XNLRRTIRLVLVAVVAVFVVCWTPIHIFILVEALGSTSHSTA-ALSSYFECIALGYINSSL 239

Db 314 NPVLVAFLEDFEKKCFRDL 333
Qy 240 NPILVAFLEDFEKKCFRDFC 259

Search completed: Thu Feb 17 11:15:49 2000
Job time : 17 secs.

(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Feb 17 11:16:07 2000; MasPar time 10.89 Seconds
Tabular output not generated. 766.047 Million cell updates/sec

Title: >US-08-455-683-12
Description: (1-295) from US08455683.pep
Perfect score: 2229
Sequence: 1 YTKMTATNIYFNALADA.....NTVQDPAYLREIDGMKNKP 295

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28258293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 48.475; Variance 96.994; scale 0.500

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2152	98.3	380	1	OPRK_HUMAN	KAPPA-TYPE OPIOID RECE	0.00e+00
2	2157	96.8	380	1	OPRK_CAVPO	KAPPA-TYPE OPIOID RECE	0.00e+00
3	2136	95.8	380	1	OPRK_MOUSE	KAPPA-TYPE OPIOID RECE	0.00e+00
4	2132	95.6	380	1	OPRK_RAT	KAPPA-TYPE OPIOID RECE	0.00e+00
5	1524	68.4	398	1	OPRM_MOUSE	MU-TYPE OPIOID RECEPTO	0.00e+00
6	1522	68.3	398	1	OPRM_RAT	MU-TYPE OPIOID RECEPTO	2.17e-282
7	1522	68.3	400	1	OPRM_HUMAN	MU-TYPE OPIOID RECEPTO	5.72e-282
8	1518	68.1	401	1	OPRM_PIG	MU-TYPE OPIOID RECEPTO	3.97e-281
9	1489	66.8	401	1	OPRM_BOVIN	MU-TYPE OPIOID RECEPTO	3.97e-281
10	1458	65.4	372	1	OPRD_HUMAN	DELTA-TYPE OPIOID RECEPTO	5.00e-275
11	1452	65.1	372	1	OPRD_RAT	DELTA-TYPE OPIOID RECEPTO	1.64e-275
12	1448	65.0	372	1	OPRD_MOUSE	DELTA-TYPE OPIOID RECEPTO	2.99e-267
13	1345	60.3	367	1	OPRX_RAT	NOCCICEPTIN RECEPTOR (O	2.07e-266
14	1343	60.3	367	1	OPRX_MOUSE	NOCCICEPTIN RECEPTOR (O	8.45e-245
15	1331	59.7	370	1	OPRX_HUMAN	NOCCICEPTIN RECEPTOR (O	2.23e-244
16	1327	59.5	370	1	OPRX_PIG	NOCCICEPTIN RECEPTOR (O	2.23e-244
17	1329	59.2	370	1	OPRX_MOUSE	NOCCICEPTIN RECEPTOR (O	5.01e-241
18	1240	55.6	228	1	OPRD_CAVPO	DELTA-TYPE OPIOID RECEPTO	2.38e-239
19	830	37.2	391	1	SSR1_RAT	SOMATOSTATIN RECEPTOR	7.95e-223
20	830	37.2	391	1	SSR1_HUMAN	SOMATOSTATIN RECEPTOR	7.95e-223
21	830	37.2	391	1	SSR1_MOUSE	SOMATOSTATIN RECEPTOR	7.95e-223
22	822	36.9	384	1	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	3.07e-136
23	816	36.6	388	1	SSR4_HUMAN	SOMATOSTATIN RECEPTOR	5.20e-135

24	810	36.3	384	1	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	8.78e-134
25	789	35.4	368	1	SSR2_BOVIN	SOMATOSTATIN RECEPTOR	1.73e-129
26	789	35.4	369	1	SSR2_PIG	SOMATOSTATIN RECEPTOR	1.73e-129
27	788	35.4	369	1	SSR2_MOUSE	SOMATOSTATIN RECEPTOR	2.76e-129
28	785	35.2	369	1	SSR2_RAT	SOMATOSTATIN RECEPTOR	1.13e-128
29	780	35.0	369	1	SSR2_HUMAN	SOMATOSTATIN RECEPTOR	1.19e-127
30	736	33.0	363	1	OPR8_HUMAN	PROBABLE G PROTEIN-COU	1.10e-118
31	696	31.2	362	1	SSR5_MOUSE	SOMATOSTATIN RECEPTOR	1.45e-110
32	683	30.6	418	1	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	6.21e-108
33	676	30.3	363	1	SSR5_HUMAN	SOMATOSTATIN RECEPTOR	1.62e-105
34	668	30.0	363	1	SSR5_RAT	SOMATOSTATIN RECEPTOR	6.69e-105
35	661	29.7	328	1	OPR7_HUMAN	PROBABLE G PROTEIN-COU	1.73e-103
36	635	28.5	98	1	OPRM_CAVPO	MU-TYPE OPIOID RECEPTO	3.01e-98
37	601	27.0	428	1	SSR3_RAT	SOMATOSTATIN RECEPTOR	2.02e-91
38	599	26.9	428	1	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	5.08e-91
39	545	24.5	349	1	GALR_HUMAN	GALANIN RECEPTOR TYPE	3.00e-80
40	525	23.6	346	1	GALR_RAT	GALANIN RECEPTOR TYPE	2.77e-76
41	521	23.4	348	1	GALR_MOUSE	GALANIN RECEPTOR TYPE	1.71e-75
42	522	23.4	372	1	GALS_RAT	GALANIN RECEPTOR TYPE	1.09e-75
43	510	22.9	402	1	GPR0_HUMAN	PROBABLE G PROTEIN-COU	2.55e-73
44	496	22.3	355	1	CKR1_HUMAN	C-C CHEMOKINE RECEPTOR	1.46e-70
45	496	22.3	359	1	AG2R_CANFA	TYPE-1 ANGIOTENSIN II	1.46e-70

ALIGNMENTS

RESULT	1	OPRK_HUMAN	STANDARD;	PRT;	380 AA.
AC	P41145;				
DT	01-FEB-1995 (REL. 31, CREATED)				
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1).				
GN	OPRK1 OR OPRK.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PLACENTA;				
RX	MEDLINE; 94338360.				
RA	MANSION E., BARE L.A., YANG D.;				
RT	"Isolation of a human kappa opioid receptor cDNA from placenta."				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PLACENTA;				
RX	MEDLINE; 95350200.				
RA	SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,				
RT	"Kappa-Opioid receptor in humans: cDNA and genomic cloning,				
RT	chromosomal assignment, functional expression, pharmacology, and				
RT	expression pattern in the central nervous system."				
RL	PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN;				
RX	MEDLINE; 95174504.				
RA	ZHU J., CHEN C., XUE J.-C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;				
RT	"Cloning of a human kappa opioid receptor from the brain."				
RL	LIFE SCI. 56:201-207(1995).				
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR				
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF				
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
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QY 241 PLYAFLENFKRCPDFCFPLKMMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 3
ID OPK_RAT MOUSE STANDARD; PRT; 380 AA.
AC P33534;
DT 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).
GN OPK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELL G.I.;
RT "Cloning and functional comparison of kappa and delta opioid
RT receptors from mouse brain.";
RL PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKEISHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RT "Structure and chromosomal mapping of genes for the mouse
RT kappa-opioid receptor and an opioid receptor homologue (MOR-C).";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95251563.
RA LIU H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,
RA LOH H.H., WEI L.N.;
RT "Cloning and promoter mapping of mouse kappa opioid receptor gene.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96084989.
RA BELKOWSKI S.M., ZHU J., LIU-CHEN L.Y., EISENSTEIN I.K.,
RA ADLER M.W., ROGERS T.J.;
RT "Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell
RT line.";
RL J. NEUROIMMUNOL. 62:113-117(1995).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, AMYGDALA,
CC MEDIAL HASENULA, HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
CC NUCLEUS).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; L11065; G348249; -
CC EMBL; D31665; G808876; -
CC EMBL; D31663; G808876; JOINED.
CC EMBL; D31664; G808876; JOINED.
CC EMBL; S77872; G998532; -
CC EMBL; S77868; G998532; JOINED.
CC EMBL; S77869; G998532; JOINED.
CC EMBL; S81111; E257489; -
CC PIR; A48227; A48227.
CC GCRDB; GCR_0635; -.

Query Match 95.88; Score 2136; DB 1; Length 380;
Best Local Similarity 92.98; Pred. No. 0.00e+00;
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;
Db 87 YTKMKTATNIYIENLALADALVITTTMPFQSAVYLMNSWPFQDLCKIVISIDYNNFTSI 146
QY 1 YTKMKTATNIYIENLALADALVITTTMPFQSAVYLMNSWPFQDLCKIVISIDYNNFTSI 60
Db 147 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIWLLSSVSGISAIVLGGTKVEDVD 206
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIWLLSSVSGISAIVLGGTKVEDVD 120
Db 207 VIECSLQEPDDDEYSWDLFKICVFVFAVPIVLIIVCYITLMILKSVRLLSGSRKD 266
QY 121 VIECSLQEPDDDEYSWDLFKICVFVFAVPIVLIIVCYITLMILKSVRLLSGSRKD 180
Db 267 RNLRRITKLVVVAVFIICWTPIHIFILVEALGSTSHSTAALSSVYFCIALGYTNSSLN 326
QY 181 XNLRRTIRLVVVAVFVVCWTFPIHIFILVEALGSTSHSTAALSSVYFCIALGYTNSSLN 240
Db 327 PVIYAFLENFKRCPDFCFPLKMMERXSTSRVNTVQDPASMRDVGGM-NKPV 380
QY 241 PLYAFLENFKRCPDFCFPLKMMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 4
ID OPK_RAT STANDARD; PRT; 380 AA.
AC P34975;
DT 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPK1 OR KOR-D.
OS RATUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94059008.
RA CHEN Y., MESTEK A., LIU J., YU L.;
RT "Molecular cloning of a rat kappa opioid receptor reveals sequence
RT similarities to the mu and delta opioid receptors.";

```

RL BIOCHEM. J. 295:625-628(1993).
RN SEQUENCE FROM N.A.
RX MEDLINE; 93374033.
RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
RA KANEKO S., SATOH M.,
RT "Cloning and expression of a cDNA for the rat kappa-opioid receptor.";
RL FEBS LETT. 329:291-295(1993).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94059009.
RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.,
RA LIU-CHEN L.-Y.,
RT "Molecular cloning and expression of a rat kappa opioid receptor.";
RL BIOCHEM. J. 295:629-633(1993).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94052210.
RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
RA WATSON S.J., AKIL H.,
RT "Cloning and pharmacological characterization of a rat kappa opioid
RT receptor.";
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=BRAIN;
RX MEDLINE; 93380375.
RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.,
RT "cDNA cloning and pharmacological characterization of an opioid
RT receptor with high affinities for kappa-subtype-selective ligands.";
RL FEBS LETT. 330:77-80(1993).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE; 95204422.
RA YAKOVLEV A.G., KRUGER K.E., FADEN A.I.,
RT "Structure and expression of a rat kappa opioid receptor gene.";
RL J. BIOL. CHEM. 270:6421-6424(1995).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; L22001; G409237; -
CC EMBL; D16829; G404116; -
CC EMBL; L22536; G425189; -
CC EMBL; U00442; G403487; -
CC EMBL; D16534; G415310; -
CC EMBL; U17995; G727260; -
CC EMBL; U17993; G727260; JOINED.
CC EMBL; U17994; G727260; JOINED.
CC PIR; S36143; S36143.
CC PIR; S38825; S38825.
CC GCRDB; GCR_0636; -
CC GCRDB; GCR_0724; -
CC GCRDB; GCR_0790; -
CC GCRDB; GCR_0804; -
CC GCRDB; GCR_1282; -
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
CC PFAM; PF00001; 7tm_1; 1.
CC G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;

KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL)
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CARBOHYD 42 42 V -> L (IN REF. 2).
FT CONFLICT 345 345 C -> Y (IN REF. 3).
SQ SEQUENCE 380 AA; 42688 MW; EE858A46 CRC32;

Query Match 95.6%; Score 2132; DB 1; Length 380;
Best Local Similarity 92.5%; Pred. No. 0.00e+00;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMTATNIYIFNLALADALVTTMPFQSAVYLMNSWPGDVLCIKIVISIDYNNFTSI 146
|||||
QY 1 YTKMTATNIYIFNLALADALVTTMPFQSTVYLMNSWPGDVLCIKIVISIDYNNFTSI 60
|||||
Db 147 FTLTMSVDRIYAVCHPVKALDPTPLKAIINICWLLASSVGISAIVLGGTKVREDVD 206
|||||
QY 61 FTLTMSVDRIYAVCHPVKALDPTPLKAIINICWLLSSSSVGISAIVLGGTKVREDVD 120
|||||
Db 207 VIECSLOFPDDEYSWDLFMKICVFVFAFVPLVLIIVCVITLMLRLKSVLLSGSREKD 266
|||||
QY 121 VIECSLOFPDDEYSWDLFMKICVFVFAFVPLVLIIVCVITLMLRLKSVLLSGSREKD 180
|||||
Db 267 RNLRRITKLVVAVFIIQWTPFIHILVEALGSTSHSTAVLSYFCIALGYTNSLN 326
|||||
QY 181 XNLRRITKLVVAVFIIQWTPFIHILVEALGSTSHSTAVLSYFCIALGYTNSLN 240
|||||
Db 327 PVLYAFIDENKRCFRFCPIKMMERQSTNRYNVTVQDPASMDYGGM-NKPV 380
|||||
QY 241 PLYAFIDENKRCFRFCPIKMMERQSTNRYNVTVQDPASMDYGGM-NKPV 295
|||||

RESULT 5
ID OPRM_MOUSE STANDARD; PRT; 398 AA.
AC P42866; G60768;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1 OR OPRM OR MOR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RC STRAIN-C57BL/6; TISSUE=LIVER;
RX MEDLINE; 94377496.
RA MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;
RT "Genomic structure analysis of promoter sequence of a mouse mu opicoid
RT receptor gene.";
RL PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 95377399.
RA ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;

"Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide receptor.";
 RL FEBS LETT. 369:192-196(1995).
 [3]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=BRAIN;
 RA MEDLINE; 95318184.
 RA KAUFMAN D.L., KEITH D.E., ANTON B., TIAN J., MAGENDZO K.,
 RA NEWMAN D., TRAN T., LEE D.S., WEN C., XIA Y., LUSIS A.J.,
 RA EVANS C.J.;
 RT "Characterization of the murine mu opioid receptor gene.";
 RL J. BIOL. CHEM. 270:15877-15883(1995).
 CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
 CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
 CC FOR BETA-ENDOPHEIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; U10561; G565069; -
 DR EMBL; U10558; G565069; JOINED.
 DR EMBL; U10559; G565069; JOINED.
 DR EMBL; U10560; G565069; JOINED.
 DR EMBL; U26915; G1055231; -
 DR EMBL; U19380; G885865; -
 DR GCRDB; GCR_1312; -
 DR GCRDB; GCR_1699; -
 DR GCRDB; GCR_1707; -
 DR MGD; MGI:97441; OPRM.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
 DR PFAM; PF00001; 7tm1; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
 FT DOMAIN 1 64
 FT TRANSMEM 65 94
 FT DOMAIN 95 103
 FT TRANSMEM 104 121
 FT DOMAIN 122 143
 FT TRANSMEM 144 163
 FT DOMAIN 164 193
 FT TRANSMEM 194 209
 FT DOMAIN 210 234
 FT TRANSMEM 235 257
 FT DOMAIN 258 280
 FT TRANSMEM 281 303
 FT DOMAIN 304 311
 FT TRANSMEM 312 328
 FT DOMAIN 329 338
 FT DISULFID 140 227
 FT LIPID 351 351
 FT CARBOHYD 9 9
 FT CARBOHYD 31 31
 FT CARBOHYD 38 38
 FT CARBOHYD 46 46
 FT CONFLICT 22 22
 FT SEQUENCE 398 AA; 44421 MW; C0211489 CRC32;
 Query Match 68.4%; Score 1524; DB 1; Length 398;
 Best Local Similarity 65.7%; Pred. No. 2.17e-282;
 Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;
 Db 96 YPKMTATNIYIFNLALADALATSLPFSVNLGMGTWPFGLCKIVISIDYNNFTSI 155
 QY 1 YPKMTATNIYIFNLALADALATSLPFSVNLGMGTWPFGLCKIVISIDYNNFTSI 60

Db 156 FTLCMTSVDRYIAVCHPVKALDFRPRNAKIVNVCNWLSSAIGLPVMMATTKYRQ-S 214
 QY 61 FTLCMTSVDRYIAVCHPVKALDFRPRNAKIVNVCNWLSSAIGLPVMMATTKYRQ-S 214
 Db 215 -IDCTLTSTSHPTW-YWENLLKICVFIEAFIMPVLLIITTCYIGIMILRLKSVMLSGSKKD 272
 QY 121 VIECQLQFPDDDDYSWDLFMKICVFIEAFIVPVLIIIVCYTILMILRLKXXVLLSGSKKD 180
 Db 273 NNLRLTRMLVWVAVFVVCWTPHIIYVIRKALIIIPETTFQTVSWHFCIALGYNSGLN 332
 QY 181 XNLRLTRMLVWVAVFVVCWTPHIIYVIRKALIIIPETTFQTVSWHFCIALGYNSGLN 332
 Db 333 PVLYAFIDENKRCFERECIFTSITIEOONSARIQNTREHPSTANTVD 381
 QY 241 PILYAFIDENKRCFERECIFTSITIEOONSARIQNTREHPSTANTVD 381
 RESULT 6
 ID OPRM_RAT STANDARD; PRT; 398 AA.
 AC P33535; Q64064; Q62846; Q64120;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 13-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE MU-TYPE OPIOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MOR1).
 GN OPRM1 OR MOR-B.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 93351652.
 RA FUKUDA K., KATO S., MORI K., NISHI M., TAKEISHIMA H.;
 RT "Primary structures and expression from cDNAs of rat opioid receptor
 RT delta- and mu-subtypes.";
 RL FEBS LETT. 327:311-314(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 94052137.
 RA WANG J.-B., IWAI Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R.;
 RT "Mu opiate receptor: cDNA cloning and expression.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 93341493.
 RA CHEN Y., MESTEK A., LIU J., HURLEY J.A., YU L.;
 RT "Molecular cloning and functional expression of a mu-opioid receptor
 RL from rat brain.";
 RL MOL. PHARMACOL. 44:8-12(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RA BUNZOW J.R., GRANDY D.K., KELLY M.;
 RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDJ DATA BANKS.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;
 RX MEDLINE; 94059560.
 RA THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
 RT "Cloning and pharmacological characterization of a rat mu opioid
 RT receptor.";
 RL NEURON 11:903-913(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 94246380.
 RA ZASTAWNY R.L., GEORGE S.R., NGUYEN T., CHENG R., TSAI S.J.,
 RA BRIONES-URBINA R., O'DOWD B.F.;
 RT "Cloning, characterization, and distribution of a mu-opioid receptor
 RT in rat brain.";
 RL J. NEUROCHEM. 62:2099-2105(1994).

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FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 46 46 POTENTIAL.
FT CARBOHYD 53 53 POTENTIAL.
FT CONFLICT 237 237 F -> G (IN REF. 6).
FT CONFLICT 245 245 V -> I (IN REF. 3, 4 AND 7).
FT CONFLICT 387 391 LENLE -> KIVLF (IN REF. 8).
SQ SEQUENCE 398 AA: 44494 MW: 2C21013D CRC32;

Query Match 68.3%; Score 1522; DB 1; Length 398;
Best Local Similarity 66.1%; Pred. No. 5,72e-282;
Matches 191; Conservative 45; Mismatches 49; Indels 4; Gaps 4;

Db 96 YIKMKATNIYFNALADALATSTLPFOSVNYLMTGTPFGTILCKIVISIDYNNFTSI 155
QY 1 YTKMKATNIYFNALADALATVTTTTPFOSVYLMNSWFGDYLCIVISIDYNNFTSI 60
Db 156 FTLLCTMSVDRIYAVCHPVKALDFTPRNAKIVNVCNMILSSAIGLPMFMFAITKYQG-S 214
QY 61 FTLLTMSVDRIYAVCHPVKALDFTPLKAKIINICIIWLLSSVGSIAVLGGTKVREDVD 120
Db 215 -IDCTTFSTPTW-YMENLLKICVFIAFIMPVLIITVCYGLMILKSVRMISGSKED 272
QY 121 VIECCLOFPDDYSWMDLFMKICVFIAFIPVLIITVCYGLMILKSVRMISGSKED 180
Db 273 RNLRRTIRMLVAVVAVFVVCVTHIIVIIKALITIPETTFQVSWHFCIALGYTNSCLN 332
QY 181 XNLRRITRLVAVVAVFVVCVTHIIFILVEALGSHSTAALSSYYFCIALGYTNSSLN 240
Db 333 PLYAFIDENFKRCFRFCIPTSTIEEQNSTRVQRNTREHPSTANTVD 381
QY 241 PLYAFIDENFKRCFRFCPLKMXMERXSTSRVR-NTVQDPAYLREID 288

RESULT 7
ID OPRM_HUMAN STANDARD; PRT; 400 AA.
AC P35372; Q12930;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1 OR MOR1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94139928.
RA WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
UHL G.R.;
RT "Human mu opiate receptor. cDNA and genomic clones, pharmacologic
characterization and chromosomal assignment.";
RL FEBS LETT. 338:217-222(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MESTEK A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,
CHEN Y., YU L.;
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 95046336.
RA BARE L.A., MANSSON E., YANG D.;
RT "Expression of two variants of the human mu opioid receptor mRNA in
SK-N-SH cells and human brain.";
RL FEBS LETT. 354:213-216(1994).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR BETA-ENDORPHIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----

Matches 185; Conservative 45; Mismatches 47; Indels 3; Gaps 3;

Db 99 YTKMKTATNIYFNALADALATSTLPFOSVNYLMTWPGTILCKIVISIDYNNFTSI 158
YTKMKTATNIYFNALADALATSTLPFOSVNYLMTWPGTILCKIVISIDYNNFTSI 158
QY 1 YTKMKTATNIYFNALADALATSTLPFOSVNYLMTWPGTILCKIVISIDYNNFTSI 60
YTKMKTATNIYFNALADALATSTLPFOSVNYLMTWPGTILCKIVISIDYNNFTSI 60
Db 159 FTLCSTVSDRYTAVCHPVKALDRTPRNAKIIINICNWLSSAIGLPMFMATTKYRQG-S 217
FTLCSTVSDRYTAVCHPVKALDRTPRNAKIIINICNWLSSAIGLPMFMATTKYRQG-S 217
QY 61 FTLTMSVDRIYLAACHPVKALDRTPLKAKIINICNWLSSVSGISAIVLGKVRDVED 120
FTLTMSVDRIYLAACHPVKALDRTPLKAKIINICNWLSSVSGISAIVLGKVRDVED 120
Db 218 -IDSTLTFTSHPTW-YWENLTKICVFIFAFITPILITVCGMLRLKSVRLMSGSKED 275
-IDSTLTFTSHPTW-YWENLTKICVFIFAFITPILITVCGMLRLKSVRLMSGSKED 275
QY 121 VIECCIQFPDDSYWDLFMKICVFIFAFIPVLIIVCYTLMILRLKXVRLSSGREK 180
VIECCIQFPDDSYWDLFMKICVFIFAFIPVLIIVCYTLMILRLKXVRLSSGREK 180
Db 276 RNLRRTRMVLVAVFIVCWTPHIIYVILKALITTPETFTQVSNHFCIALGYTNSCLN 335
RNLRRTRMVLVAVFIVCWTPHIIYVILKALITTPETFTQVSNHFCIALGYTNSCLN 335
QY 181 XNLRRTIRLVVAVFVVCWTFPHIFILVEALGSGSHSTAALSSYFFCIALGYTNSLN 240
XNLRRTIRLVVAVFVVCWTFPHIFILVEALGSGSHSTAALSSYFFCIALGYTNSLN 240
Db 336 PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 375
PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 375
QY 241 PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 280
PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 280

RESULT 10
ID OPRD HUMAN STANDARD; PRT; 372 AA.
AC P41143;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1).
GN OPRD1 OR OPRD.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
RC TISSUE-BRAIN CORTEX, AND STRIATUM;
RX MEDLINE; 94260835.
RA KNAPP R.J.; MALATYNSKA E.; FANG L.; LI X.; BABIN E.; NGUYEN M.;
SANTORO G.; VARGA E.V.; HRUBY V.J.; ROESKE W.R.; YAMAMURA H.I.;
RT "Identification of a human delta opioid receptor: cloning and
expression.";
RL LIFE SCI. 54:463-469(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95107267.
RA SIMONIN F.; BEFORT K.; GAVERIAUX-RUFF C.; MATTHES H.; NAPPEY V.;
LANNES B.; MICHELETTI G.; KIEFFER B.;
RT "The human delta-opioid receptor: genomic organization, cDNA cloning,
functional expression, and distribution in human brain.";
RL MOL. PHARMACOL. 46:1015-1021(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA GRAHAM D.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
STERESELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
[1]
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CC EMBL; U07882; G497314; -;
CC EMBL; U10504; G501145; -;
CC EMBL; AL009181; E1250368; -;
CC GCRDB; GCR_1017; -;

QY 121 VIECCIQFPDDSYWDLFMKICVFIFAFIPVLIIVCYTLMILRLKXVRLSSGREK 180
VIECCIQFPDDSYWDLFMKICVFIFAFIPVLIIVCYTLMILRLKXVRLSSGREK 180
Db 276 RNLRRTRMVLVAVFIVCWTPHIIYVILKALITTPETFTQVSNHFCIALGYTNSCLN 335
RNLRRTRMVLVAVFIVCWTPHIIYVILKALITTPETFTQVSNHFCIALGYTNSCLN 335
QY 181 XNLRRTIRLVVAVFVVCWTFPHIFILVEALGSGSHSTAALSSYFFCIALGYTNSLN 240
XNLRRTIRLVVAVFVVCWTFPHIFILVEALGSGSHSTAALSSYFFCIALGYTNSLN 240
Db 336 PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 375
PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 375
QY 241 PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 280
PLYAFLDENFKCFRFPCTSTSTBQONSTRQNTRD 280

RESULT 9
ID OPRM BOVIN STANDARD; PRT; 401 AA.
AC P79350;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
[1]
RN SEQUENCE FROM N.A.
RC TISSUE-STRIATUM;
RA SIMON E.J.; VILLEM S.; ANDRIA M.; ONOPRISHVILI I.; HILLER J.M.;
STUMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR BETA-ENDORPHIN.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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or send an email to license@isb-sib.ch).
CC EMBL; U89677; G1881731; -;
CC GCRDB; GCR_1213; -;
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm.1.1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
FT DOMAIN 1 67 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 68 97 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 98 106 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 107 124 2 (POTENTIAL).
FT TRANSMEM 125 146 3 (POTENTIAL).
FT TRANSMEM 147 166 4 (POTENTIAL).
FT TRANSMEM 167 196 5 (POTENTIAL).
FT TRANSMEM 197 212 6 (POTENTIAL).
FT TRANSMEM 213 237 7 (POTENTIAL).
FT TRANSMEM 238 260 8 (POTENTIAL).
FT TRANSMEM 261 283 9 (POTENTIAL).
FT TRANSMEM 284 306 10 (POTENTIAL).
FT TRANSMEM 307 314 11 (POTENTIAL).
FT TRANSMEM 315 331 12 (POTENTIAL).
FT TRANSMEM 332 401 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 354 354 PALMITATE (POTENTIAL).
FT LIPID 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 34 34 POTENTIAL.
FT CARBOHYD 41 41 POTENTIAL.
FT CARBOHYD 49 49 POTENTIAL.
FT CARBOHYD 49 49 POTENTIAL.
SQ SEQUENCE 401 AA; 45045 MW; 5673B9B8 CRC32;
Query Match 66.8%; Score 1489; DB 1; Length 401;
Best Local Similarity 66.1%; Pred. No. 5.00e-275;

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DR GCRDB; GCR_2055; -.
DR MM; 165195; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7tm_1; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT DOMAIN 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT DOMAIN 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372
FT CARBOHYD 18 18
FT CARBOHYD 33 33
FT DISULFID 121 198
FT LIPID 333
FT CONFLICT 27 27
FT CONFLICT 40 41
FT CONFLICT 348 348
FT CONFLICT 370 370
FT CONFLICT 370 370
FT CONFLICT 370 370
SQ SEQUENCE 372 AA; 40368 MW; 4A57DD07 CRC32;

Query Match
Best Local Similarity 65.4%; Score 1458; DB 1; Length 372;
Matches 180; Conservative 43; Mismatches 33; Indels 4; Gaps 4;

Db 77 YTKMKTATNIYIFNLALADALATSTLPFQSAKYLMTWPFGLCKAVLSIDYNNFTSI 136
QY 1 YTKMKTATNIYIFNLALADALATSTLPFQSAKYLMTWPFGLCKAVLSIDYNNFTSI 60
Db 137 FTLTMSVDRIYAVCHPVKALDFTPAKALINICIWLASGVGVPIMVAVTPRDGA- 195
QY 61 FTLTMSVDRIYAVCHPVKALDFTPAKALINICIWLASGVGVPIMVAVTPRDGA- 120
Db 196 VV-CMLOFPSPW-YVDVTYKICVFLFAVVPILLITVCYGLMLRLSRVLLSGSKED 253
QY 121 VIECLOQFPDDYDYSWMDLFMKICVFIFAFVPLVLIIVCYTLMILRLKXVLLSGSKED 180
Db 254 RSLRRTTRMVLVVGAFVVCWAPIHFEVILVTLVDIRDPLVVAALHLCIALGYANSSL 313
QY 181 XNLRITRLVVLVAVVAVVVCWAPIHFEVILVTLVDIRDPLVVAALHLCIALGYANSSL 239
Db 314 NPVLYAFDENKRCFRQLC 333
QY 240 NPVLYAFDENKRCFRDSC 259

RESULT 11
ID OPD_RAT
AC P33533;
DT 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
GN OPD1 OR ROR-A.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCUROGNATHI; MURIDAE; MORINAE; RATTUS.
EN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI K., TAKESHIMA H.;
RT "Primary structures and expression from cDNAs of rat opioid receptor
```


GN OPR1 OR OOR.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC BODENTIA; SCIUROGNATHI; MORIDAE; MORINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RX MEDLINE; 94215703.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H., IWABE N.,
RA MIYATA T., HOUTANI T., SUGIMOTO T.,
RT "cDNA cloning and regional distribution of a novel member of the
RT opioid receptor family.";
RL FEBS LETT. 343:42-46(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RA MENG F., XIE G., ALFRED M., THOMPSON R., HOVERSTEN M., WATSON S.,
RA AKIL H.,
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94307401.
RA BUNZOW J.R., SAEZ C., MORTUD M., BOUVIER C., WILLIAMS J.T., LOW M.,
RA GRANDY D.K.,
RT "Molecular cloning and tissue distribution of a putative member of
RT the rat opioid receptor gene family that is not a mu, delta or kappa
RT opioid receptor type.";
RL FEBS LETT. 347:284-288(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94307400.
RA CHEN Y., FAN Y., LIU J., MESTEK A., TIAN M., KOZAK C.A., YU L.,
RA "Molecular cloning, tissue distribution and chromosomal localization
RT of a novel member of the opioid receptor gene family.";
RL FEBS LETT. 347:279-283(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 95096849.
RA LACHOWICZ J.E., SHEN Y., MONSMA F.J. JR., SIBLEY D.R.,
RT "Molecular cloning of a novel G protein-coupled receptor related to
RT the opiate receptor family.";
RL J. NEUROCHEM. 64:34-40(1995).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94298959.
RA WANG J.B., JOHNSON P.S., IMAI Y., PERSICO A.M., OZENBERGER B.A.,
RA EPPLER C.M., UHL G.R.,
RT "cDNA cloning of an orphan opiate receptor gene family member and its
RT splice variant.";
RL FEBS LETT. 348:75-79(1994).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 95182817.
RA WICK M.J., MINNERATH S.R., LIN X., ELDE R.P., LAW P.Y., LOH H.H.,
RT "Isolation of a novel cDNA encoding a putative membrane receptor with
RT high homology to the cloned mu, delta, and kappa opioid receptors.";
RL BRAIN RES. MOL. BRAIN RES. 27:37-44(1994).
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; D16438; G533355; -
DR EMBL; U05239; G451844; -
DR EMBL; U01913; G487965; -
DR EMBL; L28144; G496220; -
DR EMBL; U07871; G606803; -
DR EMBL; L33916; G557200; -
DR EMBL; L29419; G510719; -
DR PIR; S46238; S46238; -
DR PIR; S43655; S43655; -
DR GCRDB; GCR_0834; -
DR GCRDB; GCR_0898; -
DR GCRDB; GCR_0912; -
DR GCRDB; GCR_1030; -
DR GCRDB; GCR_1455; -
DR GCRDB; GCR_1487; -
DR GCRDB; GCR_1537; -
DR PROSITE; PS00437; G_PROTEIN_RECEPTOR; 1.
DR PFAM; P349001; 7tm_1; 1.
DR HSP; P34996; 1DD0.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 84
FT TRANSMEM 85 106
FT DOMAIN 107 121
FT TRANSMEM 122 143
FT DOMAIN 144 162
FT TRANSMEM 163 185
FT DOMAIN 186 208
FT TRANSMEM 209 233
FT DOMAIN 234 261
FT TRANSMEM 262 285
FT DOMAIN 286 297
FT TRANSMEM 298 319
FT DOMAIN 320 366
FT DISULFID 120 197
FT LIPTD 331 331
FT CARBOHYD 21 21
FT CARBOHYD 26 26
FT CARBOHYD 36 36
FT CONFLICT 105 105
FT CONFLICT 226 226
FT CONFLICT 246 246
FT CONFLICT 348 348
SQ SEQUENCE 367 AA; 40523 MW; 7FD40CCC CRC32;
Query Match 60.3%; Score 1345; DB 1; Length 367;
Best Local Similarity 62.1%; Pred. No. 8.49e-245;
Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;
Db 77 TMKMTATNIYFNALADTLVLLIPFGDTLLGFWFPGNALCKTVIAIDYNNFTSTF 136
QY 2 TMKMTATNIYFNALADALVTTTFQSTVYVLMNSWPFQDLCKIVISIDYNNFTSTF 61
Db 137 TLTAMSDRYVAICHPIRALDVRTSSKAQVNVATLASVGVPAVMGSAQV-EDEE- 194
QY 62 TLTMSVDRYAVCHPVKALDFRTPKRAIKINICWLSSSVGISAIVLGSTKVEDYDV 121
Db 195 IECLVEIPAPDY-WGPVFA-ICIEFLSFIPVLLIISVCYSLMIRRLGVRLLSSREKD 252
QY 122 IECCQFDP-DDYSWMDLEFMKICVFIFAPVPLIIVCYILMILRLKXVRLSSREKD 180
Db 253 RMLRITRLVLVAVFVCGTTPVQVTVLVOGLVQVQSGEFAVAILRCTALGVYNSCLN 312
QY 181 XNLRITRLVLVAVFVCGTTPVQVTVLVOGLVQVQSGEFAVAILRCTALGVYNSCLN 240
Db 313 PILYAFLENKACPRKCCASSLHREMVDVRSIAKD 352

DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (FOR-3).
GN OPR1 OR ORL1 OR OOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN STEM;
RX MEDLINE; 94185768.
RA MOLLEREAU C., PARMENTIER M., MAILLEUX P., BUTOUR J.L., MOISAND C.,
RA CHALON P., CAPUT D., VASSART G., MEUNIER C.;
RT "ORL1, a novel member of the opioid receptor family. Cloning,
RT functional expression and localization.";
RL FEBS LETT. 341:33-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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DR EMBL; X77130; G471317; -
DR EMBL; U30185; G144297; -
DR FIR; S43087; S43087; -
DR GCRDB; GCR_0987; -
DR GCRDB; GCR_1988; -
DR MIM; 602548; -
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
DR PFAM; PF00001; 7cm_1; 1.
DR HSP; F34996; IDDD.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 50
FT TRANSMEM 51 77
FT DOMAIN 78 87
FT TRANSMEM 88 109
FT DOMAIN 110 124
FT TRANSMEM 125 146
FT DOMAIN 147 165
FT TRANSMEM 166 188
FT DOMAIN 189 211
FT TRANSMEM 212 236
FT DOMAIN 237 264
FT TRANSMEM 265 288
FT DOMAIN 289 300
FT TRANSMEM 301 322
FT DOMAIN 323 370
FT DISULFID 123 200
FT LIPID 334 334
FT CARBOHYD 21 21
FT CARBOHYD 28 28
FT CARBOHYD 39 39
SQ SEQUENCE 370 AA; 40693 MW; B53C3E8F CRC32;

Query Match 59.7%; Score 1331; DB 1; Length 370;
Best Local Similarity 60.6%; Pred. No. 7,28e-242;
Matches 171; Conservative 49; Mismatches 57; Indels 5; Gaps 5;
Db 80 TMKATATNIYFNALADALVLTITIMPFOGIVLMSNPFQGVLCCKIVISIDYNNFTSIF 139

QY 2 TKMTATNIYFNALADALVLTITIMPFOGIVLMSNPFQGVLCCKIVISIDYNNFTSIF 61
Db 140 TLTAMSDRYVAICHPIRALDVRTSSKAQAVNVAIWALASVGVPAIMGSAQV-EDEE- 197
QY 62 TLTMSVDRIAVCHPVKALDERTPLKAKINICINILLSSVGSISAVLGKVKREDVDV 121
Db 198 IECLVEIPTQDY-WGPVFA-ICIFLFSFIVPVLVISVCYSLMIRRLRGVRLSSGREK 255
QY 122 IECLQFPD-DDYSWDLFMKICVFIFAFVPLIIIVCVTLMLRLKXVRLSSGREK 180
Db 256 RNLRRITRLVAVVGVGWTVPVLAQGLGVQSPSTAVAILRFPCTALGYVNSCLN 315
QY 181 XNLRRITRLVAVVGVGWTVPVLAQGLGVQSPSTAVAILRFPCTALGYVNSCLN 240
Db 316 PILYAFLDENFKACFRKFCASALRRDQVSDRVRSIAKDVA 357
QY 241 PILYAFLDENFKACFRDCEFPKXMXMERXSTSRVNTVQDPA 282

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